



#5

SEQUENCE LISTING

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<120> Cone Snail Peptides

<130> 2314-249

<150> US 60/267,408

<151> 2001-02-09

<160> 638

<170> PatentIn version 3.0

<210> 1

<211> 290

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

<222> (4)..(231)

<400> 1

atc	atg	gag	aaa	ctg	ata	att	ctg	ctt	ctt	gtt	gct	gct	gta	ctg	atg	48
Met	Glu	Lys	Leu	Ile	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met		
1				5					10					15		

tcg	acc	cag	gcc	ctg	gtt	gaa	cgt	gct	gga	gaa	aac	cgc	tca	aag	gag	96
Ser	Thr	Gln	Ala	Leu	Val	Glu	Arg	Ala	Gly	Glu	Asn	Arg	Ser	Lys	Glu	
			20					25					30			

aac	atc	aat	ttt	tta	tta	aaa	aga	aag	aga	gct	gct	gac	agg	ggg	atg	144
Asn	Ile	Asn	Phe	Leu	Leu	Lys	Arg	Lys	Arg	Ala	Ala	Asp	Arg	Gly	Met	
			35					40					45			

tgg	ggc	gat	tgc	aaa	gat	ggg	tta	acg	aca	tgt	ttt	gcg	ccc	tca	gag	192
Trp	Gly	Asp	Cys	Lys	Asp	Gly	Leu	Thr	Thr	Cys	Phe	Ala	Pro	Ser	Glu	
			50				55					60				

tgt	tgt	tct	gag	gat	tgt	gaa	ggg	agc	tgc	acg	atg	tgg	tgatgacctc			241
Cys	Cys	Ser	Glu	Asp	Cys	Glu	Gly	Ser	Cys	Thr	Met	Trp				
			65				70					75				

tgaccacaag	ccatctgaca	tcaccactct	cctcttcaga	ggcttcaag			290
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<210> 2

<211> 76

<212> PRT
 <213> Conus ammiralis

<400> 2
 Met Glu Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu Asn
 20 25 30
 Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp
 35 40 45
 Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu Cys
 50 55 60
 Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
 65 70 75

<210> 3
 <211> 31
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 18, 22 and 25 is Glu or gamma-carboxy-Glu; Xaa at
 residue 16 is Pro or hydroxy-Pro; Xaa at residues 3 and 31 is Trp
 (D or L) or bromo-Trp (D or L)

<400> 3
 Gly Met Xaa Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Xaa
 1 5 10 15
 Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa
 20 25 30

<210> 4
 <211> 295
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (4)..(246)

<400> 4
 atc atg gag aaa ctg aca att ctg ctt ctt gtt gct gct gta ctg atg 48
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15
 tcg acc cag gcc ctg cct caa ggt ggt gga gaa aaa cgc cca agg gag 96
 Ser Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu
 20 25 30
 aat atc aga ttt tta tca aaa aga aag aca aat gct gag cgt tgg agg 144
 Asn Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg
 35 40 45

gag ggc agt tgc acc tct tgg tta gcg acg tgt acg caa gac cag caa 192
 Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln
 50 55 60

tgc tgt act gat gtt tgt tac aaa agg gac tac tgc gcc ttg tgg gat 240
 Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp
 65 70 75

gac cgc tgaccacaag ccattctgaca tcaccactct cctgttcaga gtcttcaag 295
 Asp Arg
 80

<210> 5
 <211> 81
 <212> PRT
 <213> Conus ammiralis

<400> 5
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15

Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu Asn
 20 25 30

Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg Glu
 35 40 45

Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln Cys
 50 55 60

Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp Asp
 65 70 75 80

Arg

<210> 6
 <211> 36
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 1,
 9 and 33 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 2
 5 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
 yr or O-phospho-Tyr

<400> 6
 Xaa Arg Xaa Gly Ser Cys Thr Ser Xaa Leu Ala Thr Cys Thr Gln Asp
 1 5 10 15

Gln Gln Cys Cys Thr Asp Val Cys Xaa Lys Arg Asp Xaa Cys Ala Leu
 20 25 30

Xaa Asp Asp Arg
 35

<210> 7
 <211> 275

<212> DNA
 <213> *Conus ammiralis*

<220>
 <221> CDS
 <222> (4)..(219)

<400> 7
 atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15
 tcg acc cag gcc ctg ttt caa gaa aaa cgc aca atg aag aag atc gat 96
 Ser Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp
 20 25 30
 ttt tta tca aag gga aag gca gat gct gag aag cag agg aag cgc aat 144
 Phe Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn
 35 40 45
 tgc tcg gat gat tgg cag tat tgt gaa agt ccc agt gac tgc tgt agt 192
 Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser
 50 55 60
 tgg gat tgt gat gtg gtc tgc tcg gga tgaactctga ccacaagtca 239
 Trp Asp Cys Asp Val Val Cys Ser Gly
 65 70
 tccgacatca ccactctcct gttcagaggc ttcaag 275

<210> 8
 <211> 72
 <212> PRT
 <213> *Conus ammiralis*

<400> 8
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp Phe
 20 25 30
 Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn Cys
 35 40 45
 Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser Trp
 50 55 60
 Asp Cys Asp Val Val Cys Ser Gly
 65 70

<210> 9
 <211> 25
 <212> PRT
 <213> *Conus ammiralis*

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residue 12

is Pro or hydroxy-Pro; Xaa at residues 6 and 18 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 9

Asn Cys Ser Asp Asp Xaa Gln Xaa Cys Xaa Ser Xaa Ser Asp Cys Cys
1 5 10 15

Ser Xaa Asp Cys Asp Val Val Cys Ser
20 25

<210> 10

<211> 280

<212> DNA

<213> *Conus ammiralis*

<220>

<221> CDS

<222> (4)..(246)

<400> 10

atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct cta ctg ttg 48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu
1 5 10 15

tcg atc cag gcg gta aat caa gaa aaa cac caa cgg gca aag atc aac 96
Ser Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn
20 25 30

ttg ctt tca aag aga aag cca cct gct gag cgt tgg tgg cgg tgg gga 144
Leu Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly
35 40 45

gga tgc atg gct tgg ttt ggg aaa tgt tcg aag gac tcg gaa tgt tgt 192
Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys
50 55 60

tct aat agt tgt gac ata acg cgc tgc gag tta atg cga ttc cca cca 240
Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro
65 70 75

gac tgg tgacatcgac actctcctgt tcagagtctt caag 280
Asp Trp
80

<210> 11

<211> 81

<212> PRT

<213> *Conus ammiralis*

<400> 11

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu Ser
1 5 10 15

Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
20 25 30

Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
35 40 45

Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys Ser
 50 55 60

Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro Asp
 65 70 75 80

Trp

<210> 12

<211> 39

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(39)

<223> Xaa at residues 19 and 31 is Glu or gamma-carboxy-Glu; Xaa at residues 36 and 37 is Pro or hydroxy-Pro; Xaa at residues 1, 2, 4, 10 and 39 is Trp (D or L) or bromo-Trp (D or L)

<400> 12

Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Lys Cys Ser Lys
 1 5 10 15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Ile Thr Arg Cys Xaa Leu
 20 25 30

Met Arg Phe Xaa Xaa Asp Xaa
 35

<210> 13

<211> 267

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

<222> (4)..(213)

<400> 13

atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg acg 48
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Thr
 1 5 10 15

tcg acc cag gcc ctg att caa ggt ggt gga gac gaa cgc caa aag gca 96
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Asp Glu Arg Gln Lys Ala
 20 25 30

aag atc aac ttt ctt tca agg tcg gac cgc gat tgc agg ggt tac gat 144
 Lys Ile Asn Phe Leu Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp
 35 40 45

gcg ccg tgt agc tct ggc gcg cca tgt tgt gat tgg tgg aca tgt tca 192
 Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser
 50 55 60

gca cga acc ggg cgc tgt ttt taggctgacc acaagccatc cgacatcacc 243
 Ala Arg Thr Gly Arg Cys Phe
 65 70

actctcctct tcagaggctt caag 267

<210> 14
 <211> 70
 <212> PRT
 <213> *Conus ammiralis*

<400> 14
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Thr Ser
 1 5 10 15
 Thr Gln Ala Leu Ile Gln Gly Gly Gly Asp Glu Arg Gln Lys Ala Lys
 20 25 30
 Ile Asn Phe Leu Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp Ala
 35 40 45
 Pro Cys Ser Ser Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser Ala
 50 55 60
 Arg Thr Gly Arg Cys Phe
 65 70

<210> 15
 <211> 29
 <212> PRT
 <213> *Conus ammiralis*

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residues 8 and 14 is Pro or hydroxy-Pro; Xaa at residues 1
 8 and 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-p
 hospho-Tyr

<400> 15
 Asp Cys Arg Gly Xaa Asp Ala Xaa Cys Ser Ser Gly Ala Xaa Cys Cys
 1 5 10 15
 Asp Xaa Xaa Thr Cys Ser Ala Arg Thr Gly Arg Cys Phe
 20 25

<210> 16
 <211> 277
 <212> DNA
 <213> *Conus ammiralis*

<220>
 <221> CDS
 <222> (4)..(222)

<400> 16
 atc atg cag aaa ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg 48
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15
 tcg acc cag gcc gtg ctt caa gaa aaa cgc cca aag gag aag atc aag 96
 Ser Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys
 20 25 30

ttt tta tca aag aaa aag aca gat gct gag aag cag cag aag cgc ctt 144
Phe Leu Ser Lys Lys Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu
35 40 45

tgc ccg gat tac acg gag cct tgt tca cat gcc cat gaa tgc tgt tca 192
Cys Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser
50 55 60

tgg aat tgt cat aat ggg cac tgc acg gga tgaactcgga ccacaagcca 242
Trp Asn Cys His Asn Gly His Cys Thr Gly
65 70

tcgacatcat cactctcctg ttcagagtct tcaag 277

<210> 17
<211> 73
<212> PRT
<213> Conus ammiralis

<400> 17
Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Phe
20 25 30

Leu Ser Lys Lys Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys
35 40 45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp
50 55 60

Asn Cys His Asn Gly His Cys Thr Gly
65 70

<210> 18
<211> 26
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residues 7 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 3 and 8 is Pro or hydroxy-Pro; Xaa at residue 18 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 18
Leu Cys Xaa Asp Xaa Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
1 5 10 15

Ser Xaa Asn Cys His Asn Gly His Cys Thr
20 25

<210> 19
<211> 287
<212> DNA
<213> Conus ammiralis

<220>

<221> CDS

<222> (4)..(228)

<400> 19

atc atg cag aaa ctg ata att ctg ctc ctt gtt gct gct gta ctg atg 48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
1 5 10 15

tgc acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc cgg aaa gcg 96
Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala
20 25 30

gag atc aac ttt tct aaa aca aga aat ttg gcg aga aac aag cag aaa 144
Glu Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys
35 40 45

cgc tgc agt agt tgg gca aag tat tgt gaa gtt gac tgc gaa tgc tgt 192
Arg Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys
50 55 60

tcc gaa cag tgt gta agg tct tac tgc gcg atg tgg tgatgacctc 238
Ser Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
65 70 75

tgaccacaag ccacccgata tcaccactct cctcttcaga gacttcaag 287

<210> 20

<211> 75

<212> PRT

<213> *Conus ammiralis*

<400> 20

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1 5 10 15

Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu
20 25 30

Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys Arg
35 40 45

Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys Ser
50 55 60

Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
65 70 75

<210> 21

<211> 27

<212> PRT

<213> *Conus ammiralis*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 9, 13 and 17 is Glu or gamma-carboxy-Glu; Xaa at
residue 13 is Pro or hydroxy-Pro; Xaa at residues 4 and 27 is Trp
(D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 7 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21
 Cys Ser Ser Xaa Ala Lys Xaa Cys Xaa Val Asp Ser Xaa Cys Cys Ser
 1 5 10 15
 Xaa Gln Cys Val Arg Ser Xaa Cys Ala Met Xaa
 20 25

<210> 22
 <211> 461
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (4)..(270)

<400> 22
 gtt aaa atg cat ctg tca ctg gca cgc tca gct gtt ttg atg ttg ctt 48
 Lys Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu
 1 5 10 15
 ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata 96
 Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile
 20 25 30
 aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg 144
 Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu
 35 40 45
 caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt 192
 Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys
 50 55 60
 aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc 240
 Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys
 65 70 75
 acg ttt agc gga tgc aaa att att ttg ata taaacggatt gagtttgctc 290
 Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile
 80 85
 gtcaacaaga tgtcgcacta cagctcctct ctacagtgtg tacatcgacc aaacgacgca 350
 tcttttatatt ctttgtctgt tgtatttggt ttctgtgtt cataacgtac agagcccttt 410
 aattaccttt actgctcttc acttaacctg ataaccggaa ggtccagtgc t 461

<210> 23
 <211> 89
 <212> PRT
 <213> Conus ammiralis

<400> 23
 Lys Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu
 1 5 10 15

Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr
 20 25 30
 Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln
 35 40 45
 Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn
 50 55 60
 Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr
 65 70 75 80
 Phe Ser Gly Cys Lys Ile Ile Leu Ile
 85

<210> 24
 <211> 28
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

<400> 24
 Ser Cys Asn Asn Ser Cys Asn Xaa His Ser Asp Cys Xaa Ser His Cys
 1 5 10 15
 Ile Cys Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile
 20 25

<210> 25
 <211> 459
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (7)..(270)

<400> 25
 gttaaa atg cat ctg tca ctg gca cgc tta gct gtt ttg atg ttg ctt 48
 Met His Leu Ser Leu Ala Arg Leu Ala Val Leu Met Leu Leu
 1 5 10

 ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata 96
 Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile
 15 20 25 30

 aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg 144
 Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu
 35 40 45

 caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt 192
 Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys
 50 55 60

 aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc 240

Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys
 65 70 75
 acg ttt aga gga tgc gga gct gtt aat ggt tgagtttgct cgtcaacatg 290
 Thr Phe Arg Gly Cys Gly Ala Val Asn Gly
 80 85
 atgtcgcaact acacactaca gctcctctct acagtgtgta catcgaccaa acgacgcatc 350
 ttttattttct ttgtctgttg tgtttgtttt cctgtgttca taacgtacag agccctttaa 410
 ttactttttac tgctcttcac ttaacctgat aaccagaagg tccagtgtc 459
 <210> 26
 <211> 88
 <212> PRT
 <213> *Conus ammiralis*
 <400> 26
 Met His Leu Ser Leu Ala Arg Leu Ala Val Leu Met Leu Leu Leu Leu
 1 5 10 15
 Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr Arg
 20 25 30
 Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln Ser
 35 40 45
 Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn Asn
 50 55 60
 Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr Phe
 65 70 75 80
 Arg Gly Cys Gly Ala Val Asn Gly
 85
 <210> 27
 <211> 27
 <212> PRT
 <213> *Conus ammiralis*
 <220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu
 <400> 27
 Ser Cys Asn Asn Ser Cys Asn Xaa His Ser Asp Cys Xaa Ser His Cys
 1 5 10 15
 Ile Cys Thr Phe Arg Gly Cys Gly Ala Val Asn
 20 25
 <210> 28
 <211> 387
 <212> DNA
 <213> *Conus arenatus*
 <220>

<221> CDS

<222> (19)..(240)

<400> 28

accaaaacca tcatcaaa atg aaa ctg acg tgc gtg gtg atc gtc gct gtg 51
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val
 1 5 10

ctg ttc ctg acg gcc tgt caa ctc act aca gct gat gac tcc aga ggt 99
 Leu Phe Leu Thr Ala Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly
 15 20 25

acg cag aag cat ggt gcc ctg aga tgc acc acc aaa ctc tcc atg ttg 147
 Thr Gln Lys His Gly Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu
 30 35 40

act cgg ggc tgc acg cct cct ggt gga gtt tgt ggt tat cat ggt cac 195
 Thr Arg Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His
 45 50 55

tgc tgc gat ttt tgc gat acg ttc ggc aat tta tgt gtg agt ggc 240
 Cys Cys Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser Gly
 60 65 70

tgaccgga tctgacctt ccccttctt tgcctcacta tctttttct gctgagtc 300

tccatacctg agagctgtca tgaaccactc aacacctact cttccggagg tttctgagga 360

gctgcattga aataaaagcc gcattgc 387

<210> 29

<211> 74

<212> PRT

<213> Conus arenatus

<400> 29

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Gly
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Gly Cys Thr
 35 40 45

Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys Asp Phe Cys
 50 55 60

Asp Thr Phe Gly Asn Leu Cys Val Ser Gly
 65 70

<210> 30

<211> 28

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 4 and 5 is Pro or hydroxy-Pro; Xaa at residue 11

is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 30

Gly Cys Thr Xaa Xaa Gly Gly Val Cys Gly Xaa His Gly His Cys Cys
1 5 10 15

Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser
20 25

<210> 31

<211> 375

<212> DNA

<213> *Conus arenatus*

<220>

<221> CDS

<222> (24)..(260)

<400> 31

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
Met Ser Gly Leu Gly Ile Met Val Leu Thr
1 5 10

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101
Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu
15 20 25

aag aag gcg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
Lys Lys Ala Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
30 35 40

ctc act cgg gga gta gta act gag gcg tgc gaa gag tcc tgt gag gag 197
Leu Thr Arg Gly Val Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu
45 50 55

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245
Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala
60 65 70

gtt ata tgc tgg gga tagtttctcg cacactgtct cattcattat tttatcagta 300
Val Ile Cys Trp Gly
75

caagtgtaaa cgagacatgt cagaaagtcg aagggttggtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210> 32

<211> 79

<212> PRT

<213> *Conus arenatus*

<400> 32

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Lys Ala Met Gln Arg
20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Leu Thr Arg Gly Val Val
 35 40 45

Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu Glu Glu Lys His Cys Cys
 50 55 60

His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly
 65 70 75

<210> 33

<211> 32

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 4, 7, 8, 11, 12, 13 and 14 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32 is Trp (D or L) or bromo-Trp (D or L)

<400> 33

Val Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Xaa Xaa Xaa Lys His
 1 5 10 15

Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa
 20 25 30

<210> 34

<211> 375

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (24)..(260)

<400> 34

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101
 Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu
 15 20 25

aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca 149
 Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser
 30 35 40

cgc act cgg aga ata gta act gag gcg tgc gaa gag tcc tgt gag gac 197
 Arg Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp
 45 50 55

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245
 Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala
 60 65 70

gtt ata tgc tgg gga tagtttctcg cacactgtct cattcattat tttatcagta 300
 Val Ile Cys Trp Gly

75

caagtgtaaa cgagacatgt cagaaagtcg aaggttggtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210> 35

<211> 79

<212> PRT

<213> Conus arenatus

<400> 35

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Val Phe
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Thr Glu Arg
20 25 30

Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser Arg Thr Arg Arg Ile Val
35 40 45

Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp Glu Glu Lys His Cys Cys
50 55 60

His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly
65 70 75

<210> 36

<211> 32

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32 is
Trp (D or L) or bromo-Trp (D or L)

<400> 36

Ile Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Asp Xaa Xaa Lys His
1 5 10 15

Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa
20 25 30

<210> 37

<211> 374

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (24)..(260)

<400> 37

gacaggattg aacaaaattc agg atg tca gaa ctg gga atc atg gtg cta acg 53
Met Ser Glu Leu Gly Ile Met Val Leu Thr
1 5 10


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ctt cta ctt ctt gtg ttc ctg gta acc agt cat cag gat gca gga gag      101
Leu Leu Leu Leu Val Phe Leu Val Thr Ser His Gln Asp Ala Gly Glu
      15                20                25

aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca      149
Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser
      30                35                40

ctc act cgg aga ata gta act gag gcg tgc gaa gag cac tgt gag gat      197
Leu Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu His Cys Glu Asp
      45                50                55

gag gaa cag ttc tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc      245
Glu Glu Gln Phe Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala
      60                65                70

cct gtt tgc ttc gga tagtttctgt acaactgtctc attaattatt ttatcagtac      300
Pro Val Cys Phe Gly
75

aagtgtaaac aaaacatgtc agaaagtcga aggttggtgcg tatttgataa gtattgtttg      360

ctgggacgaa cgga                                                         374

<210> 38
<211> 79
<212> PRT
<213> Conus arenatus

<400> 38
Met Ser Glu Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe
1                5                10                15

Leu Val Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Thr Glu Arg
      20                25                30

Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser Leu Thr Arg Arg Ile Val
      35                40                45

Thr Glu Ala Cys Glu Glu His Cys Glu Asp Glu Glu Gln Phe Cys Cys
      50                55                60

Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Pro Val Cys Phe Gly
65                70                75

<210> 39
<211> 32
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residues 4, 7, 8, 11, 13, 14 and 21 is Glu or gamma-carbox
      y-Glu; Xaa at residues 25 and 29 is Pro or hydroxy-Pro

<400> 39
Ile Val Thr Xaa Ala Cys Xaa Xaa His Cys Xaa Asp Xaa Xaa Gln Phe
1                5                10                15

```

Cys Cys Gly Leu Xaa Asn Gly Gln Xaa Phe Cys Ala Xaa Val Cys Phe
 20 25 30

<210> 40
 <211> 375
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (24)..(260)

<400> 40
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10
 ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101
 Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu
 15 20 25
 aag aag gtg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
 Lys Lys Val Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
 30 35 40
 cgc act cgg aga gta gta act ggg gcg tgc gaa gag cac tgt gag gac 197
 Arg Thr Arg Arg Val Val Thr Gly Ala Cys Glu Glu His Cys Glu Asp
 45 50 55
 gag gaa aag cac tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc 245
 Glu Glu Lys His Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala
 60 65 70
 cgt cta tgc tta gga tagttttctg tacactgtct tattcattat tttatcagta 300
 Arg Leu Cys Leu Gly
 75
 caagtgaaaa caaagcatgt cagaaagtcg aagggtgtgc gtatttgata agtattgttt 360
 actgggatga acgga 375

<210> 41
 <211> 79
 <212> PRT
 <213> Conus arenatus

<400> 41
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe
 1 5 10 15
 Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Lys Val Met Gln Arg
 20 25 30
 Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Arg Thr Arg Arg Val Val
 35 40 45
 Thr Gly Ala Cys Glu Glu His Cys Glu Asp Glu Glu Lys His Cys Cys
 50 55 60
 Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Arg Leu Cys Leu Gly

65 70 75

<210> 42
 <211> 32
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro

<400> 42
 Val Val Thr Gly Ala Cys Xaa Xaa His Cys Xaa Asp Xaa Xaa Lys His
 1 5 10 15
 Cys Cys Gly Leu Xaa Asn Gly Gln Xaa Phe Cys Ala Arg Leu Cys Leu
 20 25 30

<210> 43
 <211> 219
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (1)..(189)

<400> 43
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat 96
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30
 gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg 144
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45
 aat gtt cta cgt cgg tct gga tgt ccg tgg cat cct tgg tgt ggc 189
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly
 50 55 60
 tgatcggaat ccacgattgc aatgacagcc 219

<210> 44
 <211> 63
 <212> PRT
 <213> Conus arenatus

<400> 44
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30

Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45

Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly
 50 55 60

<210> 45
 <211> 9
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residues 4 and 7 is Pro or hydroxy-Pro; Xaa at residues 5
 and 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 45
 Ser Gly Cys Xaa Xaa His Xaa Xaa Cys
 1 5

<210> 46
 <211> 219
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (1)..(189)

<400> 46
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat 96
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30

gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg 144
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45

aat gtt cta cgt cgg tct gga tgt ccg tgg cgc cct tgg tgt ggc 189
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly
 50 55 60

tgatcggaat ccacgattgc aatgacagcc 219

<210> 47
 <211> 63
 <212> PRT
 <213> Conus arenatus

<400> 47
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30

Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45

Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly
 50 55 60

<210> 48

<211> 10

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(10)

<223> Xaa at residues 5 and 8 is Pro or hydroxy-Pro; Xaa at residues 6 and 9 is Trp (D or L) or bromo-Trp (D or L)

<400> 48

Ala Ser Gly Cys Xaa Xaa Arg Xaa Xaa Cys
 1 5 10

<210> 49

<211> 219

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (1)..(189)

<400> 49

atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

acc cag gtc atg gtt caa ggt gac gga gat caa cct gca ggt cga gat 96
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Gly Arg Asp
 20 25 30

gca gtt cca aga gac gat aac cca ggt gga acg agt gga aag ttc atg 144
 Ala Val Pro Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Met
 35 40 45

aat gct cta cgt caa tat gga tgt ccg gtg ggt ctt tgg tgt gac 189
 Asn Ala Leu Arg Gln Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp
 50 55 60

tgatcagaat ccacgattgc aatgacagcc 219

<210> 50

<211> 63

<212> PRT

<213> Conus arenatus

<400> 50

Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Gly Arg Asp

20 25 30
 Ala Val Pro Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Met
 35 40 45
 Asn Ala Leu Arg Gln Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp
 50 55 60

 <210> 51
 <211> 11
 <212> PRT
 <213> Conus arenatus

 <220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 5 is Pro or h
 ydroxy-Pro; Xaa at residue 9 is Trp (D or L) or bromo-Trp (D or L
); Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

 <400> 51
 Xaa Xaa Gly Cys Xaa Val Gly Leu Xaa Cys Asp
 1 5 10

 <210> 52
 <211> 210
 <212> DNA
 <213> Conus arenatus

 <220>
 <221> CDS
 <222> (1)..(180)

 <400> 52
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

 acc cag gtc atg ttt cga gat caa cct gca cgt cgt gat gca gtg cca 96
 Thr Gln Val Met Phe Arg Asp Gln Pro Ala Arg Arg Asp Ala Val Pro
 20 25 30

 aga gac gat agc cca gat gga atg agt gga ggg ttc atg aat gtc cca 144
 Arg Asp Asp Ser Pro Asp Gly Met Ser Gly Gly Phe Met Asn Val Pro
 35 40 45

 cgt cgg tct gga tgt ccg tgg caa cct tgg tgt ggc tgatcggaat 190
 Arg Arg Ser Gly Cys Pro Trp Gln Pro Trp Cys Gly
 50 55 60

 ccacgattgc aatgacagcc 210

 <210> 53
 <211> 60
 <212> PRT
 <213> Conus arenatus

 <400> 53
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser

Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

Thr Gln Ala Met Val Gln Asp Gln Pro Ala Gly Arg Asp Ala Val Pro
 20 25 30

Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Val Asn Ala Gln
 35 40 45

Arg Gln Tyr Gly Cys Pro Pro Gly Leu Trp Cys His
 50 55 60

<210> 57

<211> 11

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 5 and 6 is Pro or hydroxy-Pro; Xaa at residue 9 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 57

Xaa Xaa Gly Cys Xaa Xaa Gly Leu Xaa Cys His
 1 5 10

<210> 58

<211> 213

<212> DNA

<213> Conus aurisiacus

<220>

<221> CDS

<222> (1)..(189)

<400> 58

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

atc cct tca gat cgt gca tct gat ggc agg aat gcc gca gtc aac gag 96
 Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu
 20 25 30

aga gcg cct tgg ctg gtc cct tcg aca atc acg act tgc tgt gga tat 144
 Arg Ala Pro Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr
 35 40 45

aat ccg ggg aca atg tgc cct cct tgc agg tgc gat aat acc tgt 189
 Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys
 50 55 60

taaccacaaaa aaaaaaaaaa aaaa 213

<210> 59

<211> 63

<212> PRT

<213> Conus aurisiacus

<400> 59

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu
20 25 30

Arg Ala Pro Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr
35 40 45

Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys
50 55 60

<210> 60

<211> 30

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residues 2, 6, 17, 22 and 23 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 60

Ala Xaa Xaa Leu Val Xaa Ser Thr Ile Thr Thr Cys Cys Gly Xaa Asn
1 5 10 15

Xaa Gly Thr Met Cys Xaa Xaa Cys Arg Cys Asp Asn Thr Cys
20 25 30

<210> 61

<211> 202

<212> DNA

<213> Conus bandanus

<220>

<221> CDS

<222> (1)..(183)

<400> 61

atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96
Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
20 25 30

tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144
Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
35 40 45

aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193
Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
50 55 60

gaaggatcc

202

<210> 62
 <211> 61
 <212> PRT
 <213> Conus bandanus

<400> 62
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

<210> 63
 <211> 11
 <212> PRT
 <213> Conus bandanus
 <220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 63
 Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys
 1 5 10

<210> 64
 <211> 359
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (7)..(246)

<400> 64
 ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gcg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu
 1 5 10
 acg gcc tgt cag ctc aat aca gct gat gac tcc aga gat aag cag gag 96
 Thr Ala Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu
 15 20 25 30
 tac cgt gca gtg agg ttg aga gac gga atg cgg aat ttc aaa ggt tcc 144
 Tyr Arg Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser
 35 40 45
 aag cgc aac tgc ggg gaa caa ggt gaa ggt tgt gct act cgc cca tgc 192

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Lys Arg Asn Cys Gly Glu Gln Gly Glu Cys Ala Thr Arg Pro Cys
50 55 60
tgc tct ggt ctg agt tgc gtt ggc agc cgt cca gga ggc ctg tgc cag 240
Cys Ser Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln
65 70 75
tac ggc taatagtctg gcatctgata tttccctctt gcactctacc ttcttttgcc 296
Tyr Gly
80
tgatgcatgt ttacttgtgt gtgggtcatga accactcagt agctacacct ccgaaggacg 356
tgc 359
<210> 65
<211> 80
<212> PRT
<213> Conus characteristicus
<400> 65
Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu Thr Ala
1 5 10 15
Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu Tyr Arg
20 25 30
Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser Lys Arg
35 40 45
Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser
50 55 60
Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr Gly
65 70 75 80
<210> 66
<211> 31
<212> PRT
<213> Conus characteristicus
<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 4 and 7 is Glu or gamma-carboxy-Glu; Xaa at resid
ues 13 and 25 is Pro or hydroxy-Pro; Xaa at residue 31 is Tyr, 12
5I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 66
Asn Cys Gly Xaa Gln Gly Xaa Gly Cys Ala Thr Arg Xaa Cys Cys Ser
1 5 10 15
Gly Leu Ser Cys Val Gly Ser Arg Xaa Gly Gly Leu Cys Gln Xaa
20 25 30
<210> 67
<211> 349
<212> DNA
<213> Conus characteristicus

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<220>

<221> CDS

<222> (1)..(270)

<400> 67

atg	atg	tcg	aaa	atg	gga	gct	atg	ttt	gtc	ctt	ttg	ctt	ctt	ttc	atc	48
Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Ile	
1				5					10					15		

ctg	cca	tcc	agc	cag	cag	gaa	gga	gat	gtc	cag	gca	aga	aaa	acg	cac	96
Leu	Pro	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	His	
			20					25					30			

ctg	aag	aga	ggc	ttc	tac	ggt	act	ctg	gca	atg	tct	acc	aga	gga	tgc	144
Leu	Lys	Arg	Gly	Phe	Tyr	Gly	Thr	Leu	Ala	Met	Ser	Thr	Arg	Gly	Cys	
		35					40					45				

tct	ggc	act	tgc	cat	cgt	cgt	gag	gac	ggc	aag	tgt	cgg	ggt	act	tgc	192
Ser	Gly	Thr	Cys	His	Arg	Arg	Glu	Asp	Gly	Lys	Cys	Arg	Gly	Thr	Cys	
	50					55					60					

gac	tgc	tcc	gga	tac	agc	tat	tgt	cgc	tgc	ggc	gac	gct	cac	cat	ttt	240
Asp	Cys	Ser	Gly	Tyr	Ser	Tyr	Cys	Arg	Cys	Gly	Asp	Ala	His	His	Phe	
65					70					75					80	

tac	cga	gga	tgc	acg	tgt	tcg	tgt	caa	ggc	tgattaattg	actcttttaa	290
Tyr	Arg	Gly	Cys	Thr	Cys	Ser	Cys	Gln	Gly			
				85				90				

ctcgttgaac	gattgaaaaa	aaaaatttta	gagcaatatg	ttcgagaaaa	accgaagac	349
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<210> 68

<211> 90

<212> PRT

<213> Conus characteristicus

<400> 68

Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Ile
1				5					10					15	

Leu	Pro	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	His
			20					25					30		

Leu	Lys	Arg	Gly	Phe	Tyr	Gly	Thr	Leu	Ala	Met	Ser	Thr	Arg	Gly	Cys
		35					40					45			

Ser	Gly	Thr	Cys	His	Arg	Arg	Glu	Asp	Gly	Lys	Cys	Arg	Gly	Thr	Cys
	50					55					60				

Asp	Cys	Ser	Gly	Tyr	Ser	Tyr	Cys	Arg	Cys	Gly	Asp	Ala	His	His	Phe
65					70					75					80

Tyr	Arg	Gly	Cys	Thr	Cys	Ser	Cys	Gln	Gly						
				85				90							

<210> 69

<211> 43

<212> PRT

<213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(43)
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 2
 3, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulp
 ho-Tyr or O-phospho-Tyr

 <400> 69
 Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly
 1 5 10 15

 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30

 His Phe Xaa Arg Gly Cys Thr Cys Ser Cys Gln
 35 40

 <210> 70
 <211> 346
 <212> DNA
 <213> Conus characteristicus

 <220>
 <221> CDS
 <222> (1)..(264)

 <400> 70
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15

 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30

 cgg aag agc ggc ttc tac ggt act ctg gca atg tct gcc aga gga tgc 144
 Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys
 35 40 45

 tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc 192
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60

 gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80

 tac cga gga tgc acg tgt aca tgt taagggtgat taattgactc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

 ttgaaccgat taaaaaaaaa attagacgaa tatgttcgag aaaaccgaag ac 346

 <210> 71
 <211> 88
 <212> PRT
 <213> Conus characteristicus

 <400> 71

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys
 35 40 45
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

<210> 72
 <211> 42
 <212> PRT
 <213> Conus characteristicus
 <220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 23
 , 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
 o-Tyr or O-phospho-Tyr

<400> 72
 Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 73
 <211> 348
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

<400> 73
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 cgg aag agc ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc 144
 Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys

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          35              40              45
tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc      192
Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
    50              55              60

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt      240
Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
    65              70              75              80

tac cga gga tgc acg tgt aca tgt taagggttgat taattcgatc ttttaactcg      294
Tyr Arg Gly Cys Thr Cys Thr Cys
          85

ttgaacgatt aaaaaaaaaa ttttagacga atatgttcga gaaaaaccga agac      348

<210> 74
<211> 88
<212> PRT
<213> Conus characteristicus

<400> 74
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1              5              10              15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
          20              25              30

Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
          35              40              45

Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
          50              55              60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
    65              70              75              80

Tyr Arg Gly Cys Thr Cys Thr Cys
          85

<210> 75
<211> 42
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (1)..(42)
<223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di
      -iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 75
Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
1              5              10              15

Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
          20              25              30

His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
          35              40

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<210> 76
 <211> 349
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

<400> 76
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 ctg aag aga ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc 144
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
 35 40 45
 tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc 192
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 tac cga gga tgc acg tgt aca tgt taagggtgat taattgactc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85
 ttgaacgatt aaaaaaaaaa atttttagagc aatatgttcg agaaaaaccg aagac 349

<210> 77
 <211> 88
 <212> PRT
 <213> Conus characteristicus

<400> 77
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
 35 40 45
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

<210> 78
 <211> 42
 <212> PRT
 <213> Conus characteristicus

 <220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

 <400> 78
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

 <210> 79
 <211> 345
 <212> DNA
 <213> Conus characteristicus

 <220>
 <221> CDS
 <222> (1)..(264)

 <400> 79
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ttt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr
 1 5 10 15
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 ctg aag aga ggc ttc tac ggt act ctg gca atg tct tcc aga gga tgc 144
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys
 35 40 45
 tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc 192
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 tac cga gga tgt acg tgt aca tgt taaggttgat taattgactc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85
 ttgaacgatt aaaaaaaaaat ttagagcaat atgttcgaga aaaccgaaga c 345

 <210> 80
 <211> 88

<212> PRT
 <213> Conus characteristicus

<400> 80
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr
 1 5 10 15
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys
 35 40 45
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

<210> 81
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 23
 , 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
 o-Tyr or O-phospho-Tyr

<400> 81
 Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 82
 <211> 344
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

<400> 82
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His

20	25	30	
ctg aag agc ggc ttc tac ggt act	ctg gca atg tct gcc aga gga tgc		144
Leu Lys Ser Gly Phe Tyr Gly Thr	Leu Ala Met Ser Ala Arg Gly Cys		
35	40	45	
tct ggc act tgc cat cgt cgt caa aac ggc gag tgt cag ggt act tgc			192
Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly Thr Cys			
50	55	60	
gac tgc gac gga cac gac cat tgt gac tgc ggt gac act ctc ggt act			240
Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu Gly Thr			
65	70	75	80
tac tca gga tgc gtg tgt ata tgt taaggttgat taattgactc ttttaactcg			294
Tyr Ser Gly Cys Val Cys Ile Cys			
85			

ttgaacgatt aaaaaaattt agagcaatat gttcgagaaa aaccgaagac	344
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<210> 83

<211> 88

<212> PRT

<213> Conus characteristicus

<400> 83

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile	
1	5 10 15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His	
	20 25 30

Leu Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys	
	35 40 45

Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly Thr Cys	
	50 55 60

Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu Gly Thr	
	65 70 75 80

Tyr Ser Gly Cys Val Cys Ile Cys	
	85

<210> 84

<211> 42

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(42)

<223> Xaa at residue 13 is Glu or gamma-carboxy-Glu; Xaa at residue 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 84

Gly Cys Ser Gly Thr Cys His Arg Arg Gln Asn Gly Xaa Cys Gln Gly	
1	5 10 15

Thr Cys Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu
20 25 30

Gly Thr Xaa Ser Gly Cys Val Cys Ile Cys
35 40

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<210> 85
<211> 422
<212> DNA
<213> Conus characteristicus
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<220>
<221> CDS
<222> (7) .. (258)
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<400>      85
gttaca atg cat ctg tca ctg gca cgc tca gct gtc ttg atg ttg ctt      48
        Met His Leu Ser  Leu Ala Arg Ser  Ala Val Leu Met Leu Leu
          1              5              10
```

ctg	ctg	ttt	gcc	ttg	gac	aac	ttc	gtt	ggg	gtc	cag	cca	gga	cag	ata	96
Leu	Leu	Phe	Ala	Leu	Asp	Asn	Phe	Val	Gly	Val	Gln	Pro	Gly	Gln	Ile	
15					20					25					30	

aca aga gat gtg gac aac cgc cgt aac cgg caa tcg cga tgg aag cca 144
Thr Arg Asp Val Asp Asn Arg Arg Asn Arg Gln Ser Arg Trp Lys Pro
35 40 45

agg agt ctc ttc aag tca ctt cat aaa cga gca tcg tgt gga ggg act 192
Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr
50 55 60

tgc	acg	gaa	agt	gcc	gat	tgc	cct	tcc	acg	tgt	agt	act	tgc	tta	cat	240
Cys	Thr	Glu	Ser	Ala	Asp	Cys	Pro	Ser	Thr	Cys	Ser	Thr	Cys	Leu	His	
		65					70					75				

gct caa tgc gag tca aca tga t g t g c a c t a c a g c t c t t c t c t a c a g t 288
Ala Gln Cys Glu Ser Thr
80

gtgtacatcg accgtacgac gcatctttta tttctttggc tgtttcattc gttttcttqt 348

gttcataaca tgcggagccc ttccgttacc tctactgctc tacacttaac ctgataacca 408

gaaaatccag tact 422

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<210> 86
<211> 84
<212> PRT
<213> Conus characteristicus
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<400> 86
Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu Leu
1 5 10 15

Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile Thr Arg
20 25 30

Asp Val Asp Asn Arg Arg Asn Arg Gln Ser Arg Trp Lys Pro Arg Ser
35 40 45

Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr Cys Thr
50 55 60

Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His Ala Gln
65 70 75 80

Cys Glu Ser Thr

<210> 87

<211> 28

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 9 and 26 is Glu or gamma-carboxy-Glu; Xaa at residue 14 is Pro or hydroxy-Pro

<400> 87

Ala Ser Cys Gly Gly Thr Cys Thr Xaa Ser Ala Asp Cys Xaa Ser Thr
1 5 10 15

Cys Ser Thr Cys Leu His Ala Gln Cys Xaa Ser Thr
20 25

<210> 88

<211> 426

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (7)..(258)

<400> 88

gttaca atg cat ctg tca ctg gca cgc tca gct gtt ttg atg ttg ctt 48
Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu
1 5 10

ctg ctg ttt gcc ttg gac aac ttc gtt ggg gtc caa cca gga cag ata 96
Leu Leu Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile
15 20 25 30

act aga gat gtg gac aac cgc cgt aac ctg caa tcg cga tgg aag cca 144
Thr Arg Asp Val Asp Asn Arg Arg Asn Leu Gln Ser Arg Trp Lys Pro
35 40 45

agg agt ctc ttc aag tca ctt cat aaa cga gca tcg tgt gga ggg act 192
Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr
50 55 60

tgc acg gaa agt gcc gat tgc cct tcc acg tgt agt act tgc tta cat 240
Cys Thr Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His
65 70 75

gct caa tgc gag tga aca tgatgtcgca ctacagctct tctctacagt 288
Ala Gln Cys Glu Thr

80

gtgtacatcg accgaccgta cgacgcacatct tttattttctt tgtctgtttc attcgttttc 348
 ttgagttcat aacatgcgga gcccttccgt tacctctact gctctacact taagctgata 408
 accagaaaat ccagtact 426

<210> 89
 <211> 82
 <212> PRT
 <213> Conus characteristicus

<400> 89
 Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu Leu
 1 5 10 15
 Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile Thr Arg
 20 25 30
 Asp Val Asp Asn Arg Arg Asn Leu Gln Ser Arg Trp Lys Pro Arg Ser
 35 40 45
 Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr Cys Thr
 50 55 60
 Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His Ala Gln
 65 70 75 80
 Cys Glu

<210> 90
 <211> 25
 <212> PRT
 <213> Conus characteristicus
 <220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residues 8 and 25 is Glu or gamma-carboxy-Glu; Xaa at resi
 due 13 is Pro or hydroxy-Pro

<400> 90
 Ser Cys Gly Gly Thr Cys Thr Xaa Ser Ala Asp Cys Xaa Ser Thr Cys
 1 5 10 15
 Ser Thr Cys Leu His Ala Gln Cys Xaa
 20 25

<210> 91
 <211> 220
 <212> DNA
 <213> Conus circumcisis

<220>
 <221> CDS
 <222> (28)..(189)

<400> 91

tgtgtgtgtg tggttctggg tccagca ttt gat ggc agg aat gcc gca gtc aac 54
 Phe Asp Gly Arg Asn Ala Ala Val Asn
 1 5

gag aga gcg cct tgg acg gtc gtt ttg tcc acc acg aat tgc tgc ggt 102
 Glu Arg Ala Pro Trp Thr Val Val Leu Ser Thr Thr Asn Cys Cys Gly
 10 15 20 25

tat aat acg atg gaa ttc tgc cct gct tgc atg tgc act tat tcc tgt 150
 Tyr Asn Thr Met Glu Phe Cys Pro Ala Cys Met Cys Thr Tyr Ser Cys
 30 35 40

cca aaa aag aaa aaa cca gga aaa ggc cgc aga aac aac tgatgctcca 199
 Pro Lys Lys Lys Lys Pro Gly Lys Gly Arg Arg Asn Asn
 45 50

ggaccctctg aaccacgacg t 220

<210> 92
 <211> 54
 <212> PRT
 <213> Conus circumciscus

<400> 92
 Phe Asp Gly Arg Asn Ala Ala Val Asn Glu Arg Ala Pro Trp Thr Val
 1 5 10 15

Val Leu Ser Thr Thr Asn Cys Cys Gly Tyr Asn Thr Met Glu Phe Cys
 20 25 30

Pro Ala Cys Met Cys Thr Tyr Ser Cys Pro Lys Lys Lys Lys Pro Gly
 35 40 45

Lys Gly Arg Arg Asn Asn
 50

<210> 93
 <211> 43
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> PEPTIDE
 <222> (1)..(43)
 <223> Xaa at residue 19 is Glu or gamma-carboxy-Glu; Xaa at residues 2,
 22, 31 and 36 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D
 or L) or bromo-Trp (D or L); Xaa at residues 15 and 28 is Tyr, 12
 5I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 93
 Ala Xaa Xaa Thr Val Val Leu Ser Thr Thr Asn Cys Cys Gly Xaa Asn
 1 5 10 15

Thr Met Xaa Phe Cys Xaa Ala Cys Met Cys Thr Xaa Ser Cys Xaa Lys
 20 25 30

Lys Lys Lys Xaa Gly Lys Gly Arg Arg Asn Asn
 35 40

<210> 94
 <211> 64
 <212> PRT
 <213> Conus consors

<400> 94
 Gly Ile Phe Val Gly Val Gln Pro Glu Gln Ile Thr Arg Asp Val Asp
 1 5 10 15
 Lys Gly Tyr Ser Thr Asp Asp Gly His Asp Leu Leu Ser Leu Leu Lys
 20 25 30
 Gln Ile Ser Leu Arg Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Glu
 35 40 45
 Cys Tyr Asn Phe Cys Asp Cys Ile Gly Thr Arg Cys Glu Ala Gln Lys
 50 55 60

<210> 95
 <211> 27
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 11 and 24 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 95
 Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Xaa Cys Xaa Asn Phe Cys
 1 5 10 15
 Asp Cys Ile Gly Thr Arg Cys Xaa Ala Gln Lys
 20 25

<210> 96
 <211> 27
 <212> PRT
 <213> Conus delesstii

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 13 and 16 is Glu or gamma-carboxy-Glu; Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at residue 25 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 96
 Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa
 1 5 10 15
 Cys Cys Ser Gly Phe Cys Leu Ile Xaa Arg Cys
 20 25

<210> 97
 <211> 375
 <212> DNA
 <213> Conus distans

<220>

<221> CDS

<222> (24)..(260)

<400> 97

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40

atc act cgg aga aat gta gat cag gag tgc att gac gcc tgt cag ctg 197
 Ile Thr Arg Arg Asn Val Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu
 45 50 55

gag gac aag aat tgc tgt ggc aga aca gat gga gaa ccc aga tgt gcg 245
 Glu Asp Lys Asn Cys Cys Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala
 60 65 70

aaa atc tgc ctc gga taatttctgt acgctgtctc attcattatt tcatccgtac 300
 Lys Ile Cys Leu Gly
 75

gagtgtaaac gagacctatt agaaagtcga aggttggtgcg taatttgata agcattgttt 360

gctggggacga acgga 375

<210> 98

<211> 79

<212> PRT

<213> Conus distans

<400> 98

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
 1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
 20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Asn Val
 35 40 45

Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu Glu Asp Lys Asn Cys Cys
 50 55 60

Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala Lys Ile Cys Leu Gly
 65 70 75

<210> 99

<211> 32

<212> PRT

<213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro

 <400> 99
 Asn Val Asp Gln Xaa Cys Ile Asp Ala Cys Gln Leu Xaa Asp Lys Asn
 1 5 10 15
 Cys Cys Gly Arg Thr Asp Gly Xaa Xaa Arg Cys Ala Lys Ile Cys Leu
 20 25 30

 <210> 100
 <211> 376
 <212> DNA
 <213> Conus distans

 <220>
 <221> CDS
 <222> (24)..(260)

 <400> 100
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

 ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25

 aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40

 atc act cgg aca gaa aca gat cag gag tgc att gac atc tgt aag cag 197
 Ile Thr Arg Thr Glu Thr Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln
 45 50 55

 gag gac aag aaa tgc tgc ggc aga tca aat gga gaa ccc aca tgt gcg 245
 Glu Asp Lys Lys Cys Cys Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala
 60 65 70
 aaa atc tgc ctc gga taatttctgt acgctgtctc gttcattatt tcgtcagtag 300
 Lys Ile Cys Leu Gly
 75

 gagtttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt 360
 tgctgggatg aacgga 376

 <210> 101
 <211> 79
 <212> PRT
 <213> Conus distans

 <400> 101
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
 1 5 10 15
 Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg

	20		25		30										
Asp	Ala	Ile	Asn	Val	Ala	Pro	Gly	Thr	Ser	Ile	Thr	Arg	Thr	Glu	Thr
	35						40					45			
Asp	Gln	Glu	Cys	Ile	Asp	Ile	Cys	Lys	Gln	Glu	Asp	Lys	Lys	Cys	Cys
	50					55					60				
Gly	Arg	Ser	Asn	Gly	Glu	Pro	Thr	Cys	Ala	Lys	Ile	Cys	Leu	Gly	
65					70					75					

<210> 102
 <211> 32
 <212> PRT
 <213> Conus distans

 <220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 1, 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa
 at residue 25 is Pro or hydroxy-Pro

 <400> 102
 Xaa Thr Asp Gln Xaa Cys Ile Asp Ile Cys Lys Gln Xaa Asp Lys Lys
 1 5 10 15
 Cys Cys Gly Arg Ser Asn Gly Xaa Xaa Thr Cys Ala Lys Ile Cys Leu
 20 25 30

 <210> 103
 <211> 376
 <212> DNA
 <213> Conus distans

 <220>
 <221> CDS
 <222> (24)..(260)

 <400> 103
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

 ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25

 aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40

 atc act cgg aga gaa aca gat cag gag tgc att gac acc tgt gag cag 197
 Ile Thr Arg Arg Glu Thr Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln
 45 50 55

 gag gac aag aaa tgc tgc ggc aga aca aat gga gaa ccc gta tgt gcg 245
 Glu Asp Lys Lys Cys Cys Gly Arg Thr Asn Gly Glu Pro Val Cys Ala
 60 65 70

 aaa atc tgc ttc gga taatttctgt acgctgtctc attcataatt tcatcagttac 300

Lys Ile Cys Phe Gly
75

gagttttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt 360

tgctgggatg aacgga 376

<210> 104

<211> 79

<212> PRT

<213> Conus distans

<400> 104

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Glu Thr
35 40 45

Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln Glu Asp Lys Lys Cys Cys
50 55 60

Gly Arg Thr Asn Gly Glu Pro Val Cys Ala Lys Ile Cys Phe Gly
65 70 75

<210> 105

<211> 32

<212> PRT

<213> Conus distans

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 1, 5, 11, 13 and 24 is Glu or gamma-carboxy-Glu;
Xaa at residue 25 is Pro or hydroxy-Pro

<400> 105

Xaa Thr Asp Gln Xaa Cys Ile Asp Thr Cys Xaa Gln Xaa Asp Lys Lys
1 5 10 15

Cys Cys Gly Arg Thr Asn Gly Xaa Xaa Val Cys Ala Lys Ile Cys Phe
20 25 30

<210> 106

<211> 250

<212> DNA

<213> Conus ermineus

<220>

<221> CDS

<222> (1)..(219)

<400> 106

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

ttc act tca gat cgt gca tcg gat gac agg aat acc aac gac aaa gca 96
 Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

tct cgc ctg ctc tct cac gtt gtc agg gga tgc tgt ggt aag tat ccc 144
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Lys Tyr Pro
 35 40 45

aat gct gcc tgt cat cct tgc ggt tgt aca gtg ggt agg cca ccg tat 192
 Asn Ala Ala Cys His Pro Cys Gly Cys Thr Val Gly Arg Pro Pro Tyr
 50 55 60

tgt gac aga ccc agt ggt gga gga cgc tgatgctcca ggaccctctg 239
 Cys Asp Arg Pro Ser Gly Gly Gly Arg
 65 70

aaccacgacg t 250

<210> 107
 <211> 73
 <212> PRT
 <213> Conus ermineus

<400> 107
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Lys Tyr Pro
 35 40 45

Asn Ala Ala Cys His Pro Cys Gly Cys Thr Val Gly Arg Pro Pro Tyr
 50 55 60

Cys Asp Arg Pro Ser Gly Gly Gly Arg
 65 70

<210> 108
 <211> 30
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue7, 13, 21, 22 and 27 is Pro or hydroxy-Pro; Xaa at
 residues 6 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
 -sulpho-Tyr or O-phospho-Tyr

<400> 108
 Gly Cys Cys Gly Lys Xaa Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys
 1 5 10 15

Thr Val Gly Arg Xaa Xaa Xaa Cys Asp Arg Xaa Ser Gly Gly
 20 25 30

<210> 109
 <211> 241

<212> DNA

<213> *Conus generalis*

<220>

<221> CDS

<222> (1)..(210)

<400> 109

gga tcc atg atg tct aaa ctg gga gtc ttg ttg acc atc tgt ctg gtt	48
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val	
1 5 10 15	

ctg ttt ccc ctt act gct ctt cca ctg gat gga gaa caa cct gta gac	96
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp	
20 25 30	

cga cat gcc gag cat atg cag gat gac aat tca gct gca cag aac ccc	144
Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro	
35 40 45	

tgg gtt att gcc atc aga cag tgt tgc acg ttc tgc aac ttt gga tgc	192
Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys	
50 55 60	

cag cct tgt tgc gtc ccc tgataacgtg ttgatgacca actttctcga g	241
Gln Pro Cys Cys Val Pro	
65 70	

<210> 110

<211> 70

<212> PRT

<213> *Conus generalis*

<400> 110

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Val Pro
65 70

<210> 111

<211> 16

<212> PRT

<213> *Conus generalis*

<220>

<221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 12 and 16 is
 Pro or hydroxy-Pro

<400> 111
 Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
 1 5 10 15

<210> 112
 <211> 404
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (18)..(242)

<400> 112
 gcaagatcat cagcaga atg aac ctg acg tgc gtg ttg atc atc gcc gtg 50
 Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val
 1 5 10

ctg ttt ctg acg gcc tgc cag ctc att gca gct gat gac tcc aga gat 98
 Leu Phe Leu Thr Ala Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp
 15 20 25

aac cag aag cac cgt gca gtg agg atg aga gac gca ttg aag aat ttc 146
 Asn Gln Lys His Arg Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe
 30 35 40

aaa gat tcc agg gcg tgc tcc ggt aga ggt tct aga tgt cct ccc caa 194
 Lys Asp Ser Arg Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln
 45 50 55

tgc tgc atg ggt ttg acg tgc ggt cgt gag tat cca ccc aga tgc ggt 242
 Cys Cys Met Gly Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly
 60 65 70 75

tgatatacgg tgaacaactg atatttcccc tctgtgctct accctctttt gcttgattca 302

cccacaccta tgtgtggtca tgaaccactc agtacctaca cctctggtgg cttcagagga 362

cgtatattaa aataaaacca cattgcaatg aaaaaaaaaa aa 404

<210> 113
 <211> 75
 <212> PRT
 <213> Conus geographus

<400> 113
 Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp Asn Gln Lys His Arg
 20 25 30

Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe Lys Asp Ser Arg Ala
 35 40 45

Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly Leu
 50 55 60

Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly
 65 70 75

<210> 114
 <211> 27
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 22 is Glu or gamma-carboxy-Glu; Xaa at residues 10
 , 11, 24 and 25 is Pro or hydroxy-Pro; Xaa at residue 23 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 yr

<400> 114
 Ala Cys Ser Gly Arg Gly Ser Arg Cys Xaa Xaa Gln Cys Cys Met Gly
 1 5 10 15

Leu Thr Cys Gly Arg Xaa Xaa Xaa Xaa Arg Cys
 20 25

<210> 115
 <211> 9
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residue 7 is Pro or hydroxy-Pro

<400> 115
 Cys Phe Ile Arg Asn Cys Xaa Lys Gly
 1 5

<210> 116
 <211> 360
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)..(213)

<400> 116
 tgc tgc ccg agt agc aaa gag gat tcc ctg aac tgc att gag acc atg 48
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
 1 5 10 15

gcg acc acg gcc acg tgc atg aag tcc aac aag ggg gag atc tac tcc 96
 Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
 20 25 30

tat gcg tgc ggc tac tgc ggc aag aag aag gag agc tgt ttc ggc gac 144
 Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp


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35              40              45
aaa aag cca gtg act gac tac cag tgc cag acg cgg aac att ccc aac      192
Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
50              55              60

ccc tgc ggc ggc gct gct ctc tgaaggcacc aacagcacca acagcacgat      243
Pro Cys Gly Gly Ala Ala Leu
65              70

ctcctgtggtt tcgtcactgc atttatgacg tcaaaaccac gtcacatgcatg atgacgacga      303

tctcggctat ggcatgtatt gaagaatgga aataaaccta gttttcagct gaaaaaa      360

<210> 117
<211> 71
<212> PRT
<213> Conus geographus

<400> 117
Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
1              5              10              15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
20              25              30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp
35              40              45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
50              55              60

Pro Cys Gly Gly Ala Ala Leu
65              70

<210> 118
<211> 71
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(71)
<223> Xaa at residues 7, 14, 29 and 43 is Glu or gamma-carboxy-Glu; Xaa
      at residues 3, 51, 63 and 65 is Pro or hydroxy-Pro; Xaa at resid
      ues 31, 33, 37 and 55 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
      r, O-sulpho-Tyr or O-phospho-Tyr

<400> 118
Cys Cys Xaa Ser Ser Lys Xaa Asp Ser Leu Asn Cys Ile Xaa Thr Met
1              5              10              15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Xaa Ile Xaa Ser
20              25              30

Xaa Ala Cys Gly Xaa Cys Gly Lys Lys Lys Xaa Ser Cys Phe Gly Asp
35              40              45

Lys Lys Xaa Val Thr Asp Xaa Gln Cys Gln Thr Arg Asn Ile Xaa Asn
50              55              60

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Xaa Cys Gly Gly Ala Ala Leu
65 70

<210> 119
<211> 769
<212> DNA
<213> Conus geographus

<220>

<221> misc_feature
<222> (1)..(769)
<223> n is unknown

<400> 119
cgggcgctgc attccggacg tgaaacagca tcgccagcaa gtgggcatag tgcaagacac 60
tcagaacaat gacgcacata gtctganaaa ataaccatgg gtatgcggat gangtttagt 120
gtgtttcngc aggttgtcnt gggnaaccact gtcgtttcct tcacntcacg tcgtggtcca 180
aaatctcgtc gcggggaacc tattccgacc actgtaatca actacgggga gtgctgtaag 240
gatccatcct gttgggttaa ggtgaaggat ttccagtgtc ctggagcaag tcctcccaac 300
tgaaccacga catgtcgccc tctgcctgac ctgcttcacg ttccgtctct ttctgccact 360
agaactcaac aactcgatcc aacagactcc tactttacct ccgtattctg aaactacttg 420
gatttgattg tctttaatat ctactcacac ttgctgttat tacatcatcc aaaatttaac 480
aagaacatga aaggtgtctg ttcaaacaaa atcaggcaat gacaangggg gaaagtctcc 540
antctatctg aaaactgtca cctgtcactc tcttaaccag gtttanaact gantaccact 600
anagctgttg tnccacatca ngatcagncc aatttgtann gtttcctttg caaaactttt 660
gcctgaaatt cttgaaaaga aacgctcaca atgttgggaa gtgctttttna ttanctgaca 720
anntgncanc atgttcntt tcantaantc tnaaatgnaa acctctgtt 769

<210> 120
<211> 68
<212> PRT
<213> Conus geographus

<400> 120
Met Gly Met Arg Met Met Phe Ser Val Phe Leu Gln Val Val Leu Gly
1 5 10 15
Thr Thr Val Val Ser Phe Thr Ser Arg Arg Gly Pro Lys Ser Arg Arg
20 25 30
Gly Glu Pro Ile Pro Thr Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys
35 40 45
Asp Pro Ser Cys Trp Val Lys Val Lys Asp Phe Gln Cys Pro Gly Ala
50 55 60

Ser Pro Pro Asn
65

<210> 121
<211> 36
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residues 2 and 13 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 5, 18, 30, 35 and 35 is Pro or hydroxy-Pro; Xaa at residue 21 is Trp (D or L) or bromo-Trp (D or L);

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 121
Gly Xaa Xaa Ile Xaa Thr Thr Val Ile Asn Xaa Gly Xaa Cys Cys Lys
1 5 10 15

Asp Xaa Ser Cys Xaa Val Lys Val Lys Asp Phe Gln Cys Xaa Gly Ala
20 25 30

Ser Xaa Xaa Asn
35

<210> 122
<211> 519
<212> DNA
<213> Conus geographus

<220>
<221> CDS
<222> (113)..(391)

<400> 122
agccttgata cagagctggt atctgctggt aatacttgaa agaacaagtg ctgtgagcct 60

tcattctctct ctgacttttag tttgggtcct ggagaaaacc ttgacgggca gt atg aaa 118
Met Lys
1

att tac ctg tgt ctt gct ttt gtt ctg ctc ctg gct tct acc ata gtt 166
Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr Ile Val
5 10 15

gat tca ggg ctt ctt gat aaa att gag act ata aga aac tgg aaa cgc 214
Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp Lys Arg
20 25 30

gat gac agc tat tgt gat gga tgc cta tgc acc ata tta aaa aaa gag 262
Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Glu
35 40 45 50

act tgc aca tcg act atg agc tgc agg gga aca tgc cga aaa gag tgg 310
 Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Glu Trp
 55 60 65

cca tgt tgg gaa gaa gac tgc tac tgt act gaa atc caa ggt gga gct 358
 Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly Gly Ala
 70 75 80

tgc gtc aca ccc tca gaa tgc aaa cct gga gag tgttgaggat tggagtggcc 411
 Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu
 85 90

agttccagca catacagcac catggtgccc tggacaatcg tctattgaat tgaatatgcc 471

tgtggcagga atctgtccta caaaataaaa aaatcataag ttaaaaaa 519

<210> 123

<211> 93

<212> PRT

<213> Conus geographus

<400> 123

Met Lys Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr
 1 5 10 15

Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp
 20 25 30

Lys Arg Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys
 35 40 45

Lys Glu Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys
 50 55 60

Glu Trp Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly
 65 70 75 80

Gly Ala Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu
 85 90

<210> 124

<211> 60

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(60)

<223> Xaa at residues 16, 36, 37, 43, 56 and 59 is Glu or gamma-carboxy
 -Glu; Xaa at residues 33, 52 and 57 is Pro or hydroxy-Pro; Xaa at
 residues 32 and 35 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(60)

<223> Xaa at residues 4 and 40 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
 -Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 124

Asp Asp Ser Xaa Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Xaa

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1              5              10              15
Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Xaa Xaa
      20              25              30
Xaa Cys Xaa Xaa Xaa Asp Cys Xaa Cys Thr Xaa Ile Gln Gly Gly Ala
      35              40              45
Cys Val Thr Xaa Ser Xaa Cys Lys Xaa Gly Xaa Cys
      50              55              60

<210> 125
<211> 409
<212> DNA
<213> Conus geographus

<220>
<221> CDS
<222> (17)..(313)

<400> 125
aacgttgacg ggcagt atg aac att tac ctg tgt ctt gct ttt ctt ctg ttc      52
          Met Asn Ile Tyr Leu Cys Leu Ala Phe Leu Leu Phe
              1              5              10

ctg cct tct acc ata gtt gat tca ggg ctt ctt gat aaa att gag aca      100
Leu Pro Ser Thr Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr
      15              20              25

ata agg aat tgg aga cgt gat gaa agc aag tgt gat cga tgc aat tgc      148
Ile Arg Asn Trp Arg Arg Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys
      30              35              40

gcc gaa tta aga tca tcc aga tgc aca caa gct atc ttc tgc ctt aca      196
Ala Glu Leu Arg Ser Ser Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr
      45              50              55              60

ccg gag tta tgc aca ccg agc atc tca tgt ccg aca ggt gaa tgc cgc      244
Pro Glu Leu Cys Thr Pro Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg
      65              70              75

tgt act aag ttc cat cag tca aga tgc act aga ttc gta gaa tgc gta      292
Cys Thr Lys Phe His Gln Ser Arg Cys Thr Arg Phe Val Glu Cys Val
      80              85              90

cct aat aag tgt aga gac gca tagaggccag ttccagcaca tacagcacca      343
Pro Asn Lys Cys Arg Asp Ala
      95

tgatgccctg gacaatcgtg ttgttgatt gaatatgccc gtggcaggaa tctgtcctac      403

aaaaaa      409

<210> 126
<211> 99
<212> PRT
<213> Conus geographus

<400> 126
Met Asn Ile Tyr Leu Cys Leu Ala Phe Leu Leu Phe Leu Pro Ser Thr

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1	5	10	15
Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp	20	25	30
Arg Arg Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg	35	40	45
Ser Ser Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys	50	55	60
Thr Pro Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe	65	70	75
His Gln Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys	85	90	95

Arg Asp Ala

<210> 127
 <211> 65
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(65)
 <223> Xaa at residues 2, 12, 28, 40 and 56 is Glu or gamma-carboxy-Glu;
 Xaa at residues 27, 32, 37 and 59 is Pro or hydroxy-Pro

<400> 127
Asp Xaa Ser Lys Cys Asp Arg Cys Asn Cys Ala Xaa Leu Arg Ser Ser
1 5 10 15

Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Xaa Xaa Leu Cys Thr Xaa
20 25 30

Ser Ile Ser Cys Xaa Thr Gly Xaa Cys Arg Cys Thr Lys Phe His Gln
35 40 45

Ser Arg Cys Thr Arg Phe Val Xaa Cys Val Xaa Asn Lys Cys Arg Asp
50 55 60

Ala
65

<210> 128
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residues 9 and 23 is Glu or gamma-carboxy-Glu; Xaa at residue 28 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 128
Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Xaa Cys
1 5 10 15

Ala Lys Gly Ile Ala Lys Xaa Phe Cys Asn Cys Xaa Asp
 20 25

<210> 129
 <211> 7
 <212> PRT
 <213> Conus imperialis

<220>
 <221> PEPTIDE
 <222> (1)..(7)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 6 is Trp (D or L) or bromo-Trp (D or L)

<400> 129
 Xaa Cys Gly Gln Ala Xaa Cys
 1 5

<210> 130
 <211> 524
 <212> DNA
 <213> Conus imperialis

<220>
 <221> CDS
 <222> (7)..(285)

<400> 130
 gttaaa atg cat ctg tca ctg gca agc tca gct gct ttg atg ttg ctt 48
 Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu
 1 5 10

ctg ctt ttt gcc ttg ggc aac ttc gtt ggg gtc cag cca gga caa ata 96
 Leu Leu Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile
 15 20 25 30

aga gat ctg aac aaa gga cag ctc aag gac aac cgc cgt aac ctg caa 144
 Arg Asp Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln
 35 40 45

tcg cag agg aaa caa atg agt ctc ctc aag tca ctt cat gat cga aat 192
 Ser Gln Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn
 50 55 60

ggg tgt aac ggc aac acg tgt tcc aat agc ccc tgc cct aac aac tgt 240
 Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys
 65 70 75

tat tgc gat act gag gac gac tgc cac cct gac agg cgt gaa cat 285
 Tyr Cys Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His
 80 85 90

tagagattag agagtttcct tgtcaacatg atgtcgcacc acacctctgc tctgcagtgt 345

gtacatcgac cagtcgacgc atctgttatt tctttgtctg ttggattgta catcgaccag 405

tccacgcacg tggtatttct ttgtctgttt gatttgtttt cgtgtgttca taacacacag 465

agcctttcta ttatctgtat tgcaatacac tttgcctgat aaccagaaag tccagtgc 524

<210> 131
 <211> 93
 <212> PRT
 <213> Conus imperialis

<400> 131
 Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu Leu Leu
 1 5 10 15
 Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile Arg Asp
 20 25 30
 Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln Ser Gln
 35 40 45
 Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn Gly Cys
 50 55 60
 Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys Tyr Cys
 65 70 75 80
 Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His
 85 90

<210> 132
 <211> 32
 <212> PRT
 <213> Conus imperialis

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 22 and 31 is Glu or gamma-carboxy-Glu; Xaa at residues 13, 14 and 27 is Pro or hydroxy-Pro; Xaa at residue 18 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 132
 Asn Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Xaa Cys Xaa Asn Asn
 1 5 10 15
 Cys Xaa Cys Asp Thr Xaa Asp Asp Cys His Xaa Asp Arg Arg Xaa His
 20 25 30

<210> 133
 <211> 350
 <212> DNA
 <213> Conus lacterculatus

<220>
 <221> CDS
 <222> (1)..(273)

<400> 133
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac 96


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Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
      20      25      30
ccg aag aga gag ttc cat cgt att ctg cta agg cct gac aga cag tcc      144
Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser
      35      40      45
gaa acg gct tgt agg tcg ctc gga agc tac caa tgt atg ggt aaa tgc      192
Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys
      50      55      60
caa ctc ggg gtt cat tcc tgg tgt gaa tgc att tat aac cga ggt agt      240
Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser
      65      70      75      80
cag aag tct gga tgc gcg tgt agg tgt caa aag tgattaattg actcatttaa      293
Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
      85      90
ctcgttgaac gatttaaaaa atccagagca atatgttcga gaaaaaccga agacgac      350

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<210> 134
<211> 91
<212> PRT
<213> Conus lacterculatus

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<400> 134
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1      5      10      15
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
      20      25      30
Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser
      35      40      45
Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys
      50      55      60
Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser
      65      70      75      80
Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
      85      90

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<210> 135
<211> 45
<212> PRT
<213> Conus lacterculatus

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<220>
<221> PEPTIDE
<222> (1)..(45)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 3 and 27 is
      Glu or gamma-carboxy-Glu; Xaa at residue 25 is Trp (D or L) or br
      omo-Trp (D or L); Xaa at residues 12 and 30 is Tyr, 125I-Tyr, mon
      o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 135
Xaa Ser Xaa Thr Ala Cys Arg Ser Leu Gly Ser Xaa Gln Cys Met Gly

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1              5              10              15
Lys Cys Gln Leu Gly Val His Ser Xaa Cys Xaa Cys Ile Xaa Asn Arg
                20                25                30

Gly Ser Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
                35                40                45

<210> 136
<211> 318
<212> DNA
<213> Conus lividus

<220>
<221> CDS
<222> (7)..(237)

<400> 136
ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg      48
      Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
        1              5              10

acg gcc agt cag ctc att aca gct gat tac tcc aga gat aag cag gag      96
Thr Ala Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Lys Gln Glu
15              20              25              30

tat cgt gca gag agg ctg aga gac gca atg ggg aaa ttc aaa ggt tcc      144
Tyr Arg Ala Glu Arg Leu Arg Asp Ala Met Gly Lys Phe Lys Gly Ser
              35              40              45

agg tcg tgc gga cat agt ggt gca ggt tgt tat act cgc cct tgc tgc      192
Arg Ser Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys
              50              55              60

cct ggt ctg cat tgc tct ggc ggc caa gct gga ggc ctg tgc gtg      237
Pro Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val
              65              70              75

taatagtaat aatctggcgt ctgatatttc cagtctgtgc tctaccctct tttgcctgag      297

tcatccatac ctgtgctcga g      318

<210> 137
<211> 77
<212> PRT
<213> Conus lividus

<400> 137
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1              5              10              15

Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Lys Gln Glu Tyr Arg
                20                25                30

Ala Glu Arg Leu Arg Asp Ala Met Gly Lys Phe Lys Gly Ser Arg Ser
                35                40                45

Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys Pro Gly
                50                55                60

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Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val
 65 70 75

<210> 138
 <211> 30
 <212> PRT
 <213> Conus lividus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residues 13 and 16 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 138
 Ser Cys Gly His Ser Gly Ala Gly Cys Xaa Thr Arg Xaa Cys Cys Xaa
 1 5 10 15

Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val
 20 25 30

<210> 139
 <211> 312
 <212> DNA
 <213> Conus lividus

<220>
 <221> CDS
 <222> (7)..(252)

<400> 139
 ggatcc atg aaa ctg acg tgt gtg gtg atc ata tcc gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ser Val Leu Phe Leu
 1 5 10

acg gcc agt gag ttc ctt aca gct gat tac tcc aga gat aag cgg cag 96
 Thr Ala Ser Glu Phe Leu Thr Ala Asp Tyr Ser Arg Asp Lys Arg Gln
 15 20 25 30

tac cgt gct gtg agg ttg aga gac gca atg cgg aat ttc aaa ggt acc 144
 Tyr Arg Ala Val Arg Leu Arg Asp Ala Met Arg Asn Phe Lys Gly Thr
 35 40 45

agg gac tgc ggg gaa tca ggt caa ggt tgc tat agt gta cgt cct tgc 192
 Arg Asp Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys
 50 55 60

tgc cct ggt ctg att tgc aaa ggc acc ggt ggt gga ggc ctg tgc cgg 240
 Cys Pro Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg
 65 70 75

ccc tct ggc atc tgatatctcc cctctgtgct ccaccctctt ttgcctgagt 292
 Pro Ser Gly Ile
 80

catccataacc tgtgctcgag 312

<210> 140
 <211> 82

<212> PRT
 <213> Conus lividus

<400> 140
 Met Lys Leu Thr Cys Val Val Ile Ile Ser Val Leu Phe Leu Thr Ala
 1 5 10 15
 Ser Glu Phe Leu Thr Ala Asp Tyr Ser Arg Asp Lys Arg Gln Tyr Arg
 20 25 30
 Ala Val Arg Leu Arg Asp Ala Met Arg Asn Phe Lys Gly Thr Arg Asp
 35 40 45
 Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys Pro
 50 55 60
 Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro Ser
 65 70 75 80
 Gly Ile

<210> 141
 <211> 35
 <212> PRT
 <213> Conus lividus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residues 14,
 17 and 32 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-
 Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 141
 Asp Cys Gly Xaa Ser Gly Gln Gly Cys Xaa Ser Val Arg Xaa Cys Cys
 1 5 10 15
 Xaa Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Xaa
 20 25 30
 Ser Gly Ile
 35

<210> 142
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is
 Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 142
 Val Xaa Xaa Thr His Xaa
 1 5

<210> 143
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is
 Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo
 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 143
 Arg Xaa Lys Asn Ser Xaa
 1 5

<210> 144
 <211> 7
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(7)
 <223> Xaa at residue 2 is Pro or hydroxy-Pro; Xaa at residue 6 is Trp (
 D or L) or bromo-Trp (D or L)

<400> 144
 Ala Arg Xaa Lys Asn Ser Xaa
 1 5

<210> 145
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp (
 D or L) or bromo-Trp (D or L)

<400> 145
 Arg Xaa Lys Asn Ser Xaa
 1 5

<210> 146
 <211> 360
 <212> DNA
 <213> Conus miles

<220>
 <221> CDS
 <222> (7)..(270)

<400> 146
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtc gcc gtg ctg ttc ctg
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag 96
 Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln
 15 20 25 30

gag tac ccc gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac 144
 Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp
 35 40 45

ttg acg ttg acc aag aaa tgc acg gac gat tct cag ttc tgt aac cct 192
 Leu Thr Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro
 50 55 60

tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac 240
 Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn
 65 70 75

ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt 290
 Gly Ile Cys Ala Ile Val Pro Glu Asn Ser
 80 85

tccccctctg tgctccgccg tccgtggcct gactcgtcca tccttgggcg tgggtcatgaa 350

ccgctcggtt 360

<210> 147
 <211> 88
 <212> PRT
 <213> Conus miles

<400> 147
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr
 20 25 30

Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr
 35 40 45

Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn
 50 55 60

His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile
 65 70 75 80

Cys Ala Ile Val Pro Glu Asn Ser
 85

<210> 148
 <211> 36
 <212> PRT
 <213> Conus miles

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residues 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at res
 idues 10 and 33 is Pro or hydroxy-Pro

<400> 148

Cys Thr Asp Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys
1 5 10 15

Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val
20 25 30

Xaa Xaa Asn Ser
35

<210> 149

<211> 357

<212> DNA

<213> Conus miles

<220>

<221> CDS

<222> (7)..(270)

<400> 149

ggatcc atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag 96
Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln
15 20 25 30

gag tac cct gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac 144
Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp
35 40 45

ctg acg ttg acc aag aaa tgc acg gag gat tct cag ttc tgt aac cct 192
Leu Thr Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro
50 55 60

tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac 240
Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn
65 70 75

ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt 290
Gly Ile Cys Ala Ile Val Pro Glu Asn Ser
80 85

tccccctctg tgctccgccg tccgtggcct gactcgtcca tccttggggcg tggatcatgaa 350

ccgctcg 357

<210> 150

<211> 88

<212> PRT

<213> Conus miles

<400> 150

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr
20 25 30

Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr

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35          40          45
Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn
.    50          55          60

His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile
65          70          75          80

Cys Ala Ile Val Pro Glu Asn Ser
          85

<210> 151
<211> 36
<212> PRT
<213> Conus miles

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residues 3, 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at
      residues 10 and 33 is Pro or hydroxy-Pro

<400> 151
Cys Thr Xaa Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys
1          5          10          15

Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val
          20          25          30

Xaa Xaa Asn Ser
          35

<210> 152
<211> 327
<212> DNA
<213> Conus miliaris

<220>
<221> CDS
<222> (12)..(239)

<400> 152
ggatccatga a ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg acg          50
          Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr

          1          5          10

gcc tgt caa ctc act aca gct gtg act tcc tcc aga ggt caa cag aag          98
Ala Cys Gln Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys
          15          20          25

cat cgt gct ctg agg tca act gac aaa aac tcc agg atg acc aag cgt          146
His Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg
30          35          40          45

tgc acg cct cca ggt gga ctc tgt tac cat gct tat ccc tgc tgc agc          194
Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser
          50          55          60

aag act tgc aat ctc gat acc agc caa tgt gag cct agg tgg tca          239
Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser

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65 70 75
 tgaaccactc aataccctct cctctggagg cttcagagga actacattga aataaaaccg 299
 cattgcaacg aaaaaaaaaa aaaaaaaaaa 327

<210> 153
 <211> 76
 <212> PRT
 <213> Conus miliaris

<400> 153
 Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala Cys Gln
 1 5 10 15
 Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys His Arg Ala
 20 25 30
 Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg Cys Thr Pro
 35 40 45
 Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser Lys Thr Cys
 50 55 60
 Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser
 65 70 75

<210> 154
 <211> 31
 <212> PRT
 <213> Conus miliaris

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 27 is Glu or gamma-carboxy-Glu; Xaa at residues 3,
 4, 13 and 28 is Pro or hydroxy-Pro; Xaa at residue 30 is Trp (D
 or L) or bromo-Trp (D or L); Xaa at residues 9 and 12 is Tyr, 125
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 154
 Cys Thr Xaa Xaa Gly Gly Leu Cys Xaa His Ala Xaa Xaa Cys Cys Ser
 1 5 10 15
 Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Xaa Xaa Arg Xaa Ser
 20 25 30

<210> 155
 <211> 193
 <212> DNA
 <213> Conus monachus

<220>
 <221> CDS
 <222> (28)..(162)

<400> 155
 tgtgtgtgtg tggttctggg tccagca tct gat gtc agg aat gcc gca gtc cac 54
 Ser Asp Val Arg Asn Ala Ala Val His
 1 5

gaa aga cag aag gat ctg gtc gtt acg gcc acc acg act tgc tgt ggt 102
 Glu Arg Gln Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly
 10 15 20 25

tat aat ccg atg aca atg tgc cct cct tgc atg tgc act aat acc tgc 150
 Tyr Asn Pro Met Thr Met Cys Pro Pro Cys Met Cys Thr Asn Thr Cys
 30 35 40

aaa aaa agt ggc tgatgctcca ggaccctctg aaccacgacg t 193
 Lys Lys Ser Gly
 45

<210> 156
 <211> 45
 <212> PRT
 <213> Conus monachus

<400> 156
 Ser Asp Val Arg Asn Ala Ala Val His Glu Arg Gln Lys Asp Leu Val
 1 5 10 15

Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asn Pro Met Thr Met Cys
 20 25 30

Pro Pro Cys Met Cys Thr Asn Thr Cys Lys Lys Ser Gly
 35 40 45

<210> 157
 <211> 33
 <212> PRT
 <213> Conus monachus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 17, 22 and 23 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 157
 Xaa Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asn
 1 5 10 15

Xaa Met Thr Met Cys Xaa Xaa Cys Met Cys Thr Asn Thr Cys Lys Lys
 20 25 30

Ser

<210> 158
 <211> 350
 <212> DNA
 <213> Conus monachus

<220>
 <221> CDS
 <222> (1)..(282)

<400> 158
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48

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Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1          5          10          15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca agc      96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
          20          25          30

ctg aag agc gac ttc tat cgt gct ctg aga ggg tat gac aga cag tgc      144
Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys
          35          40          45

act ctt gtc aac aat tgt gac cgg aac ggt gag cgt gcg tgt aac ggt      192
Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly
          50          55          60

gat tgc tct tgc gag ggc cag att tgt aaa tgc ggt tat aga gtc agt      240
Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser
        65          70          75          80

cct ggg aag tca gga tgc gcg tgt act tgt aga aat gcc aaa      282
Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
          85          90

tgaatcattt aactcgttga aagattttttt aaaaatccag agctatatgt tcgagaaaaa      342

ccgaagac      350

<210> 159
<211> 94
<212> PRT
<213> Conus monachus

<400> 159
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1          5          10          15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
          20          25          30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys
          35          40          45

Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly
          50          55          60

Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser
        65          70          75          80

Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
          85          90

<210> 160
<211> 48
<212> PRT
<213> Conus monachus

<220>
<221> PEPTIDE
<222> (1)..(48)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 13 and 23 is

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Glu or gamma-carboxy-Glu; Xaa at residue 35 is Pro or hydroxy-Pro; Xaa at residue 31 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 160

Xaa Cys Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Xaa Arg Ala Cys
1 5 10 15

Asn Gly Asp Cys Ser Cys Xaa Gly Gln Ile Cys Lys Cys Gly Xaa Arg
20 25 30

Val Ser Xaa Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
35 40 45

<210> 161

<211> 211

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(192)

<400> 161

atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96
Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
20 25 30

ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144
Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
35 40 45

cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt cgt 192
Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
50 55 60

taaccagcat gaaggatcc 211

<210> 162

<211> 64

<212> PRT

<213> Conus pennaceus

<400> 162

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
50 55 60

<210> 163
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 163
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Arg
 1 5 10

<210> 164
 <211> 450
 <212> DNA
 <213> Conus pennaceus

<220>
 <221> CDS
 <222> (1)..(234)

<400> 164
 atg ttg ctt ctg ctg ttt gcc ttg ggc agc ttc gtt gtg gtc cag tca 48
 Met Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser
 1 5 10 15

gga cag ata aca aga gat gtg gac aat ggg cag ctc gcg gac aac cgc 96
 Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg
 20 25 30

cgt acc ctg cga tcg cag tgg aag caa gtg agt ttc ttc aag tca ctt 144
 Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu
 35 40 45

gat aaa cga ctg act tgt aac gat cct tgc cag atg cat tcc gat tgc 192
 Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys
 50 55 60

ggc ata tgt gaa tgc gtg gaa aat aaa tgc ata ttt ttc atg 234
 Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met
 65 70 75

taaacggatt gagtttgctt gtcaacacaa tgtcgcactg cagctcttct ctaccggtgg 294

gtacatcgac caaacgacgc atcttttatt tctttgtctg tttcgtttgt tctcctgtgt 354

tcataacgta cagagccctt taactaccct tactgtctctt cacttaacct gataacctga 414

aggtccggtg cagctggcgt agccttcaca gtttcg 450

<210> 165
 <211> 78
 <212> PRT
 <213> Conus pennaceus

<400> 165
 Met Leu Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser
 1 5 10 15

Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg
20 25 30

Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu
35 40 45

Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys
50 55 60

Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met
65 70 75

<210> 166

<211> 27

<212> PRT

<213> Conus pennaceus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 17 and 20 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro

<400> 166

Leu Thr Cys Asn Asp Xaa Cys Gln Met His Ser Asp Cys Gly Ile Cys
1 5 10 15

Xaa Cys Val Xaa Asn Lys Cys Ile Phe Phe Met
20 25

<210> 167

<211> 413

<212> DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (1)..(243)

<400> 167

atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg acg gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgt caa ctc agt aca gct gat gac tcc aga gat gag cag cag gat cct 96
Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro
20 25 30

ttg gtg agg tcg cat cgt gag gag cag aaa gcc gag gac ccc aag acg 144
Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr
35 40 45

gcc gag aga tgt tca gat ttc gga tcc gac tgt gtt cct gct act cat 192
Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His
50 55 60

aac tgc tgc agt ggt gaa tgt ttt ggc ttc gag gac ttc ggc tta tgc 240
Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys
65 70 75 80

acg taaaactggt ctgacgtctg atattccccc ctctgtcctt catcctcttt 293
Thr

tgcctgattc atccatacct atatgtgctc ctgaaccgct gtgtaccttt accctggtgg 353

cttcagagga cggtatatca aaataaaaacc gcgttgcaat gacaaaaaaaa aaaaaaaaaa 413

<210> 168

<211> 81

<212> PRT

<213> Conus pulicarius

<400> 168

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro
20 25 30

Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr
35 40 45

Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His
50 55 60

Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys
65 70 75 80

Thr

<210> 169

<211> 30

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residues 19 and 24 is Glu or gamma-carboxy-Glu; Xaa at residue 10 is Pro or hydroxy-Pro

<400> 169

Cys Ser Asp Phe Gly Ser Asp Cys Val Xaa Ala Thr His Asn Cys Cys
1 5 10 15

Ser Gly Xaa Cys Phe Gly Phe Xaa Asp Phe Gly Leu Cys Thr
20 25 30

<210> 170

<211> 375

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (24)..(260)

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<400> 170
gacaggattg aacaaaattc agg atg tca aga ttt gga atc atg gtg cta acc      53
                Met Ser Arg Phe Gly Ile Met Val Leu Thr
                  1                5                10

ttt cta ctt ctt gtg tcc atg gca acc agc cat cgt tat gca aga ggg      101
Phe Leu Leu Leu Val Ser Met Ala Thr Ser His Arg Tyr Ala Arg Gly
                15                20                25

aag cag gcg acg cga agg aac gca atc aac atc aga cgg aga agc aca      149
Lys Gln Ala Thr Arg Arg Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr
                30                35                40

cca aaa act gag gcg tgc gaa gag gtc tgt gag ctg gaa gaa aag cac      197
Pro Lys Thr Glu Ala Cys Glu Glu Val Cys Glu Leu Glu Glu Lys His
                45                50                55

tgc tgc tgc ata aga agt gac gga ccc aaa tgt tcc cgt aag tgc ctg      245
Cys Cys Cys Ile Arg Ser Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu
                60                65                70

ttg tca atc ttc tgt tagtttctgt acactgtctc attcattatc ttatcagttac      300
Leu Ser Ile Phe Cys
75

aagtgtaaac gagacatgtc agaaagtcga aggttggtgcg taatttgata agtattgttt      360

gctgggatga acgga                                                    375

<210> 171
<211> 79
<212> PRT
<213> Conus purpurascens

<400> 171
Met Ser Arg Phe Gly Ile Met Val Leu Thr Phe Leu Leu Leu Val Ser
1                5                10                15

Met Ala Thr Ser His Arg Tyr Ala Arg Gly Lys Gln Ala Thr Arg Arg
                20                25                30

Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr Pro Lys Thr Glu Ala Cys
                35                40                45

Glu Glu Val Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser
                50                55                60

Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu Leu Ser Ile Phe Cys
65                70                75

<210> 172
<211> 37
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(37)
<223> Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carboxy-Gl
u; Xaa at residues 3 and 25 is Pro or hydroxy-Pr

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<400> 172

Xaa Lys Thr Xaa Ala Cys Xaa Xaa Val Cys Xaa Leu Xaa Xaa Lys His
 1 5 10 15
 Cys Cys Cys Ile Arg Ser Asp Gly Xaa Lys Cys Ser Arg Lys Cys Leu
 20 25 30

Leu Ser Ile Phe Cys
 35

<210> 173

<211> 373

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (24)..(260)

<400> 173

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ctt cta ctt ctt gtg tcc atg gca acc aac cat cag gat aga gga gag 101
 Leu Leu Leu Leu Val Ser Met Ala Thr Asn His Gln Asp Arg Gly Glu
 15 20 25

aag cag gtg acg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
 Lys Gln Val Thr Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
 30 35 40

atc acc cag caa gtc gta tct gag gag tgc aaa aag tac tgt aag aaa 197
 Ile Thr Gln Gln Val Val Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys
 45 50 55

cag aac aag aat tgc tgc agc agt aaa cat gaa gaa ccc aga tgt gcc 245
 Gln Asn Lys Asn Cys Cys Ser Ser Lys His Glu Glu Pro Arg Cys Ala
 60 65 70

aag ata tgc ttc gga tagtttctgt acacggtctc attcattatt ttatcagtag 300
 Lys Ile Cys Phe Gly
 75

aagttaaacg agacctatca gaagtcgaag gttgtgcata atttgataaa cattgtttgc 360

tgggatgaac gga 373

<210> 174

<211> 79

<212> PRT

<213> Conus purpurascens

<400> 174

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser
 1 5 10 15

Met Ala Thr Asn His Gln Asp Arg Gly Glu Lys Gln Val Thr Gln Arg
 20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Ile Thr Gln Gln Val Val
 35 40 45

Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys Gln Asn Lys Asn Cys Cys
 50 55 60

Ser Ser Lys His Glu Glu Pro Arg Cys Ala Lys Ile Cys Phe Gly
 65 70 75

<210> 175

<211> 32

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 4, 5, 23 and 24 is Glu or gamma-carboxy-Glu; Xaa
 at residue 25 is Pro or hydroxy-Pro; Xaa at residue 9 is Tyr, 125
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 175

Val Val Ser Xaa Xaa Cys Lys Lys Xaa Cys Lys Lys Gln Asn Lys Asn
 1 5 10 15

Cys Cys Ser Ser Lys His Xaa Xaa Xaa Arg Cys Ala Lys Ile Cys Phe
 20 25 30

<210> 176

<211> 24

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 8 is Glu or gamma-carboxy-Glu; Xaa at residue 12 i
 s Pro or hydroxy-Pro; Xaa at residue 22 is Tyr, 125I-Tyr, mono-io
 do-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176

Asp Cys Cys Gly Val Lys Leu Xaa Met Cys His Xaa Cys Leu Cys Asp
 1 5 10 15

Asn Ser Cys Lys Asn Xaa Gly Lys
 20

<210> 177

<211> 235

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (1)..(204)

<400> 177

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc act tca gat cgt gca tcg gat gac agg aat acc aac gac aaa gca 96
 Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

tct cgc ctg ctc tct cac gtt gtc agg gga tgc tgt ggt agc tat ccc 144
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro
 35 40 45

aat gct gcc tgt cat cct tgc ggt tgt aaa gat agg cca tcg tat tgt 192
 Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys
 50 55 60

ggt caa gga cgc tgatgctcca ggaccctctg aaccacgacg t 235
 Gly Gln Gly Arg
 65

<210> 178
 <211> 68
 <212> PRT
 <213> Conus purpurascens

<400> 178
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro
 35 40 45

Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys
 50 55 60

Gly Gln Gly Arg
 65

<210> 179
 <211> 25
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residues 7, 13 and 20 is Pro or hydroxy-Pro; Xaa at residues 6 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 179
 Gly Cys Cys Gly Ser Xaa Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys
 1 5 10 15

Lys Asp Arg Xaa Ser Xaa Cys Gly Gln
 20 25

<210> 180
 <211> 229
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (1)..(198)

<400> 180
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 ttc acc gta gat cgt gca act gat ggc agg agt gct gca gcc ata gcg 96
 Phe Thr Val Asp Arg Ala Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala
 20 25 30
 ttt gcc ctg atc gct ccg acc gtc cgg gaa gga tgc tgt tct aat cct 144
 Phe Ala Leu Ile Ala Pro Thr Val Arg Glu Gly Cys Cys Ser Asn Pro
 35 40 45
 gcc tgt cat cct tgc ggt tgt aaa gat agg cca tcg tat tgt ggt caa 192
 Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys Gly Gln
 50 55 60
 gga cgc tgatgctcca ggaccctctg aaccacgacg t 229
 Gly Arg
 65

<210> 181
 <211> 66
 <212> PRT
 <213> Conus purpurascens

<400> 181
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Phe Thr Val Asp Arg Ala Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala
 20 25 30
 Phe Ala Leu Ile Ala Pro Thr Val Arg Glu Gly Cys Cys Ser Asn Pro
 35 40 45
 Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys Gly Gln
 50 55 60
 Gly Arg
 65

<210> 182
 <211> 23
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residues 7,
 11 and 18 is Pro or hydroxy-Pro; Xaa at residue 20 is Tyr, 125I-T
 yr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 182

Xaa Gly Cys Cys Ser Asn Xaa Ala Cys His Xaa Cys Gly Cys Lys Asp
 1 5 10 15

Arg Xaa Ser Xaa Cys Gly Gln
 20

<210> 183

<211> 334

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (1)..(261)

<400> 183

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30

ctg acg agg gac ttc tat cgt act ctg cca gtg tct act aga gga tgc 144
 Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys
 35 40 45

agc ggc tcc cct tgt ttt aaa aac aaa acg tgt cgg gat gaa tgc ata 192
 Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile
 50 55 60

tgc ggc ggc tta tcc aat tgt tgg tgt ggc tac ggc ggt agt cga gga 240
 Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly
 65 70 75 80

tgc aag tgt aca tgt aga gag tgattaatcg actctttaac tcgttgaatt 291
 Cys Lys Cys Thr Cys Arg Glu
 85

atttaaaaaa tccagagcaa tatgttcgag aaaaaccgaa gac 334

<210> 184

<211> 87

<212> PRT

<213> Conus purpurascens

<400> 184

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30

Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys
 35 40 45

Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile
 50 55 60

Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly
65 70 75 80

Cys Lys Cys Thr Cys Arg Glu
85

<210> 185

<211> 41

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 26 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 185

Gly Cys Ser Gly Ser Xaa Cys Phe Lys Asn Lys Thr Cys Arg Asp Xaa
1 5 10 15

Cys Ile Cys Gly Gly Leu Ser Asn Cys Xaa Cys Gly Xaa Gly Gly Ser
20 25 30

Arg Gly Cys Lys Cys Thr Cys Arg Xaa
35 40

<210> 186

<211> 327

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (29)..(256)

<400> 186

cgacctcaag agggatcgat agcagttc atg atg tct aaa ctg gga gcc ttg 52
Met Met Ser Lys Leu Gly Ala Leu
1 5

ttg acc atc tgt ctg ctt ctg ttt ccc att act gct ctt ctg atg gat 100
Leu Thr Ile Cys Leu Leu Leu Phe Pro Ile Thr Ala Leu Leu Met Asp
10 15 20

gga gat caa cct gca gac cga cct gca gaa cgt atg gat tac gac att 148
Gly Asp Gln Pro Ala Asp Arg Pro Ala Glu Arg Met Asp Tyr Asp Ile
25 30 35 40

tca tct gag gtg cat cgt ttg ctt gaa agg aga cac ccg ccc tgt tgc 196
Ser Ser Glu Val His Arg Leu Leu Glu Arg Arg His Pro Pro Cys Cys
45 50 55

atg tac ggc aga tgc cgt cga tat ccc gga tgc tct agt gcc tct tgt 244
Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys Ser Ser Ala Ser Cys
60 65 70

tgc cag gga gga taacgtgttg atgaccaact ttgttacacg gctacgtcaa 296

Cys Gln Gly Gly
75

gtgtctactg aataagtaaa acgattgcag t

327

<210> 187

<211> 76

<212> PRT

<213> Conus purpurascens

<400> 187

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Asp Tyr Asp Ile Ser Ser Glu Val His Arg Leu Leu
35 40 45

Glu Arg Arg His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr
50 55 60

Pro Gly Cys Ser Ser Ala Ser Cys Cys Gln Gly Gly
65 70 75

<210> 188

<211> 24

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residues 2, 3 and 14 is Pro or hydroxy-Pro; Xaa at residues 7 and 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 188

His Xaa Xaa Cys Cys Met Xaa Gly Arg Cys Arg Arg Xaa Xaa Gly Cys
1 5 10 15

Ser Ser Ala Ser Cys Cys Gln Gly
20

<210> 189

<211> 24

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residues 2, 3, 12 and 14 is Pro or hydroxy-Pro; Xaa at residues 7 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 189

Gly Xaa Xaa Cys Cys Leu Xaa Gly Ser Cys Arg Xaa Phe Xaa Gly Cys
1 5 10 15

Xaa Asn Ala Leu Cys Cys Arg Lys
20

<210> 190
<211> 400
<212> DNA
<213> *Conus quercinus*

<220>
<221> CDS
<222> (7)..(237)

<400> 190
ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gtg ctg ttt ctg 48
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
1 5 10

aca gcc agt cag ctg gtt aca gct gat tac acc aga gat aaa tgg caa 96
Thr Ala Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln
15 20 25 30

tac cct gca gcg agt ttg aga ggc gga atg tgg aat ttg aga gat acc 144
Tyr Pro Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr
35 40 45

agg gcg tgc tcg caa gta ggt gaa gct tgt ttt cct cag aaa cct tgc 192
Arg Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys
50 55 60

tgc cct gga ttc ctt tgc aat cac atc gga ggc atg tgc cac cac 237
Cys Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
65 70 75

tagtaacagt ctggcatctg atattttcccc tctgcgctcc accctctttt ggctgattca 297

tccttacctg tgtgtggtca tgaaccactc agtagctaca cctctggtgg cttcagagga 357

cgtatatcaa aataaaaacca cattgcaaaa aaaaaaaaaa aaa 400

<210> 191
<211> 77
<212> PRT
<213> *Conus quercinus*

<400> 191
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln Tyr Pro
20 25 30

Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr Arg Ala
35 40 45

Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys Pro
50 55 60

Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
65 70 75

<210> 192
 <211> 30
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residues 11,
 14 and 17 is Pro or hydroxy-Pro

<400> 192
 Ala Cys Ser Gln Val Gly Xaa Ala Cys Phe Xaa Gln Lys Xaa Cys Cys
 1 5 10 15
 Xaa Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
 20 25 30

<210> 193
 <211> 11
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 4 is Pro or hydroxy-Pro

<400> 193
 Asp Cys Gln Xaa Cys Gly His Asn Val Cys Cys
 1 5 10

<210> 194
 <211> 336
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (2)..(241)

<400> 194
 c atg aac tgt ctc gta ctg gct ttg gtt acc atc ggt ctt ctg gct gca 49
 Met Asn Cys Leu Val Leu Ala Leu Val Thr Ile Gly Leu Leu Ala Ala
 1 5 10 15
 aca acc gca gcc cct ctg gac acc acc acg gtc ctc ctc agc aca act 97
 Thr Thr Ala Ala Pro Leu Asp Thr Thr Thr Val Leu Leu Ser Thr Thr
 20 25 30
 aca cgc gat gtc aag ggc tgt gtg tac gag ggc ata gag tac agt gtc 145
 Thr Arg Asp Val Lys Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val
 35 40 45
 gga gag acc tac cag gca gac tgc aac acg tgt cgc tgt gat ggc ttt 193
 Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe
 50 55 60
 gac ctg gct aca tgc acc gtc gcg ggc tgc aca ggc ttt gga ccc gag 241

Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
65 70 75 80

tgattggtac tattccacac ctagcaatgt tcacactgga accggaactt gatactacct 301

tctaaatata atcaatttgc ttcaaaaggc ccaaa 336

<210> 195

<211> 80

<212> PRT

<213> *Conus radiatus*

<400> 195

Met Asn Cys Leu Val Leu Ala Leu Val Thr Ile Gly Leu Leu Ala Ala
1 5 10 15

Thr Thr Ala Ala Pro Leu Asp Thr Thr Thr Val Leu Leu Ser Thr Thr
20 25 30

Thr Arg Asp Val Lys Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val
35 40 45

Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe
50 55 60

Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
65 70 75 80

<210> 196

<211> 43

<212> PRT

<213> *Conus radiatus*

<220>

<221> PEPTIDE

<222> (1)..(43)

<223> Xaa at residues 5, 8, 13 and 43 is Glu or gamma-carboxy-Glu; Xaa at residue 42 is Pro or hydroxy-Pro; Xaa at residues 4,9 and 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 196

Gly Cys Val Xaa Xaa Gly Ile Xaa Xaa Ser Val Gly Xaa Thr Xaa Gln
1 5 10 15

Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe Asp Leu Ala Thr Cys
20 25 30

Thr Val Ala Gly Cys Thr Gly Phe Gly Xaa Xaa
35 40

<210> 197

<211> 536

<212> DNA

<213> *Conus radiatus*

<220>

<221> CDS

<222> (87)..(296)

<210>	198
<211>	70
<212>	PRT
<213>	Conus radiatus

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<400>      198
Met  Ser  Gly  Leu  Gly  Ile  Met  Val  Leu  Thr  Leu  Leu  Leu  Leu  Val  Ser
 1              5              10              15

Met  Ala  Thr  Ser  Arg  Gln  Asp  Arg  Gly  Val  Gly  Gln  Leu  Met  Pro  Arg
 20              25              30

Val  Ser  Phe  Lys  Ala  Cys  Lys  Ser  Asn  Tyr  Asp  Cys  Pro  Gln  Arg  Phe
 35              40              45

Lys  Cys  Cys  Ser  Tyr  Thr  Trp  Asn  Gly  Ser  Ser  Gly  Tyr  Cys  Lys  Arg
 50              55              60

Val  Cys  Tyr  Leu  Tyr  Arg
65              70

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<210> 199
<211> 34
<212> PRT
<213> Conus radiatus
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<220>
<221>  PEPTIDE
<222>  (1)..(34)
<223>  Xaa at residue 9 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp
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(D or L) or bromo-Trp (D or L); Xaa at residues 6, 17 and 33 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 199

Ala Cys Lys Ser Asn Xaa Asp Cys Xaa Gln Arg Phe Lys Cys Cys Ser
1 5 10 15

Xaa Thr Xaa Asn Gly Ser Ser Gly Xaa Cys Lys Arg Val Cys Xaa Leu
20 25 30

Xaa Arg

<210> 200

<211> 356

<212> DNA

<213> *Conus radiatus*

<220>

<221> CDS

<222> (1)..(279)

<400> 200

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac 96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

ccg aag aga gag ttc caa cgt att ctg cta agg tct ggc aga aag tgc 144
Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys
35 40 45

aat ttc gac aaa tgt aaa ggt acc gga gtc tac aat tgt ggg gaa tcc 192
Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser
50 55 60

tgc tca tgc gaa ggt ttg cac agt tgt cgc tgc act tat aac atc ggt 240
Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly
65 70 75 80

tct atg aag tct gga tgc gcg tgt att tgt aca tac tat taatgattaa 289
Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
85 90

ttgactcggt taactcggtg aacgatttaa aaaatccaga gcaatatggt cgagaaaaac 349

cgaagac 356

<210> 201

<211> 93

<212> PRT

<213> *Conus radiatus*

<400> 201

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30

Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys
 35 40 45

Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser
 50 55 60

Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly
 65 70 75 80

Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
 85 90

<210> 202

<211> 47

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(47)

<223> Xaa at residues 17 and 22 is Glu or gamma-carboxy-Glu; Xaa at residues 13, 31, 46 and 47 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 202

Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Xaa Asn Cys Gly
 1 5 10 15

Xaa Ser Cys Ser Cys Xaa Gly Leu His Ser Cys Arg Cys Thr Xaa Asn
 20 25 30

Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Xaa Xaa
 35 40 45

<210> 203

<211> 338

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (1)..(264)

<400> 203

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

ctg gca tcc agg cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
 Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30

ctg acg agc gac ttc tat agt gtt ctg caa agg tat gga cta gga tgc 144
 Leu Thr Ser Asp Phe Tyr Ser Val Leu Gln Arg Tyr Gly Leu Gly Cys
 35 40 45

gct ggc act tgt ggt tca agc agc aat tgt gtt aga gat tat tgt gac 192

Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val Arg Asp Tyr Cys Asp
50 55 60

tgc cca aaa ccc aat tgt tac tgc act ggc aaa ggc ttt cgt caa cca 240
Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys Gly Phe Arg Gln Pro
65 70 75 80

gga tgc ggg tgt tca tgt ttg ggg tgattaattg gctcttttaa ctcgttgaac 294
Gly Cys Gly Cys Ser Cys Leu Gly
85

gatttaaaaa atccagagca atatgttcga gaaaaaccga agac 338

<210> 204
<211> 88
<212> PRT
<213> Conus radiatus

<400> 204
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30

Leu Thr Ser Asp Phe Tyr Ser Val Leu Gln Arg Tyr Gly Leu Gly Cys
35 40 45

Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val Arg Asp Tyr Cys Asp
50 55 60

Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys Gly Phe Arg Gln Pro
65 70 75 80

Gly Cys Gly Cys Ser Cys Leu Gly
85

<210> 205
<211> 44
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(44)
<223> Xaa at residues 23, 25 and 37 is Pro or hydroxy-Pro; Xaa at resid
ues 1, 19 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
sulpho-Tyr or O-phospho-Tyr

<400> 205
Xaa Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val
1 5 10 15

Arg Asp Xaa Cys Asp Cys Xaa Lys Xaa Asn Cys Xaa Cys Thr Gly Lys
20 25 30

Gly Phe Arg Gln Xaa Gly Cys Gly Cys Ser Cys Leu
35 40

<210> 206

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<211> 375
<212> DNA
<213> Conus sponsalis
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<220>
<221> CDS
<222> (24) .. (260)
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[illegible]

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<210> 207
<211> 79
<212> PRT
<213> Conus sponsalis
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<400> 207															
Met	Ser	Gly	Leu	Gly	Ile	Met	Val	Leu	Thr	Leu	Leu	Leu	Leu	Val	Ser
1				5					10					15	
Met	Ala	Thr	Ser	His	Lys	Asp	Gly	Gly	Glu	Lys	Gln	Ala	Met	Gln	Arg
			20					25					30		
Asp	Ala	Ile	Asn	Val	Arg	Leu	Arg	Arg	Ser	Leu	Thr	Arg	Arg	Ala	Val
		35					40					45			
Thr	Glu	Ala	Cys	Thr	Glu	Asp	Cys	Lys	Thr	Gln	Asp	Lys	Lys	Cys	Cys
	50					55					60				
Gly	Glu	Met	Asn	Gly	Gln	His	Thr	Cys	Ala	Lys	Ile	Cys	Leu	Gly	
65					70					75					

<210>	208
<211>	32

<212> PRT
 <213> *Conus sponsalis*

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 4, 8 and 20 is Glu or gamma-carboxy-Glu

<400> 208
 Ala Val Thr Xaa Ala Cys Thr Xaa Asp Cys Lys Thr Gln Asp Lys Lys
 1 5 10 15

Cys Cys Gly Xaa Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu
 20 25 30

<210> 209
 <211> 8
 <212> PRT
 <213> *Conus stercusmuscarum*

<220>
 <221> PEPTIDE
 <222> (1)..(8)
 <223> Xaa at residues 3 and 6 is Pro or hydroxy-Pro; Xaa at residue 4 is D-Trp

<400> 209
 Gly Cys Xaa Xaa Gln Xaa Val Cys
 1 5

<210> 210
 <211> 9
 <212> PRT
 <213> *Conus striatus*

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residue 7 is Pro or hydroxy-Pro

<400> 210
 Cys Ile Ile Arg Asn Cys Xaa Arg Gly
 1 5

<210> 211
 <211> 238
 <212> DNA
 <213> *Conus striatus*

<220>
 <221> CDS
 <222> (4)..(96)

<400> 211
 agg tgc act cgc tgc ttg cct gac gga acg tct tgc ctt ttt agt agg 48
 Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
 1 5 10 15

atc aga tgc tgc ggt act tgc agt tca atc tta aag tca tgt gtg agc 96
 Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser

	20	25	30	
tgatccagcg gttgatcttc ctccctctgt gctccatcct tttctgcctg agttctcctt				156
acctgagagt ggtcatgaac cactcatcac ctactcttct ggaggcttca gaggagctac				216
agtgaaataa aagccgcatt gc				238
<210> 212				
<211> 31				
<212> PRT				
<213> Conus striatus				
<400> 212				
Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile				
1 5 10 15				
Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser				
20 25 30				
<210> 213				
<211> 28				
<212> PRT				
<213> Conus striatus				
<220>				
<221> PEPTIDE				
<222> (1)..(28)				
<223> Xaa at residue 3 is Pro or hydroxy-Pro				
<400> 213				
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys				
1 5 10 15				
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser				
20 25				
<210> 214				
<211> 707				
<212> DNA				
<213> Conus striatus				
<220>				
<221> CDS				
<222> (171)..(539)				
<400> 214				
cggttcttaa tacgactcac tatagggcaa gcagtggtaa caacgcagag tacgcggggg				60
gacggcagac cagctgggga ccagacagac gtcaaacagc atcgcagtca ggtgtggaga				120
tccaagaca cccagaagaa ggagacagaa gagttatcgt tcgtaacaca atg gcc				176
			Met Ala	
			1	
atg aac atg tcg atg aca ctc tgc atg ttt gta atg gtc gtc gtc gca				224
Met Asn Met Ser Met Thr Leu Cys Met Phe Val Met Val Val Val Ala				
5 10 15				
gcc act gtc att gat tcc act cag tta caa gaa cca gat ctc agt cgc				272

Ala	Thr	Val	Ile	Asp	Ser	Thr	Gln	Leu	Gln	Glu	Pro	Asp	Leu	Ser	Arg		
20						25					30						
atg	cga	cgc	agc	ggg	cct	gct	gac	tgt	tgc	agg	atg	aaa	gag	tgt	tgc		320
Met	Arg	Arg	Ser	Gly	Pro	Ala	Asp	Cys	Cys	Arg	Met	Lys	Glu	Cys	Cys		
35					40					45					50		
acc	gac	aga	gtg	aac	gag	tgt	cta	cag	cgc	tat	tct	ggc	cgg	gaa	gat		368
Thr	Asp	Arg	Val	Asn	Glu	Cys	Leu	Gln	Arg	Tyr	Ser	Gly	Arg	Glu	Asp		
				55					60					65			
aaa	ttc	gtt	tcg	ttt	tgt	tat	cag	gag	gcc	aca	gtc	aca	tgt	gga	tct		416
Lys	Phe	Val	Ser	Phe	Cys	Tyr	Gln	Glu	Ala	Thr	Val	Thr	Cys	Gly	Ser		
			70					75					80				
ttt	aac	gaa	atc	gtg	ggc	tgt	tgc	tat	gga	tat	caa	atg	tgc	atg	ata		464
Phe	Asn	Glu	Ile	Val	Gly	Cys	Cys	Tyr	Gly	Tyr	Gln	Met	Cys	Met	Ile		
		85					90					95					
cga	gtt	gtg	aaa	ccg	aac	agt	cta	agt	ggg	gcc	cat	gag	gcg	tgc	aaa		512
Arg	Val	Val	Lys	Pro	Asn	Ser	Leu	Ser	Gly	Ala	His	Glu	Ala	Cys	Lys		
	100					105					110						
acc	gtt	tct	tgt	ggt	aac	cct	tgc	gct	tgaggtgtcc	tcgcgccacg							559
Thr	Val	Ser	Cys	Gly	Asn	Pro	Cys	Ala									
115					120												
tcacctgtgt	acagcgccgt	caccagagcc	ctgatcttta	tgcccttata	tgtctttttg												619
ctcttttact	ctctgaagtc	ttgaggtttg	ttccattctt	gtcaatcata	tcacgcgcac												679
ccaagtaaat	aaaggtgacg	tgacaaac															707

<210> 215
 <211> 123
 <212> PRT
 <213> Conus striatus

<400> 215
 Met Ala Met Asn Met Ser Met Thr Leu Cys Met Phe Val Met Val Val
 1 5 10 15
 Val Ala Ala Thr Val Ile Asp Ser Thr Gln Leu Gln Glu Pro Asp Leu
 20 25 30
 Ser Arg Met Arg Arg Ser Gly Pro Ala Asp Cys Cys Arg Met Lys Glu
 35 40 45
 Cys Cys Thr Asp Arg Val Asn Glu Cys Leu Gln Arg Tyr Ser Gly Arg
 50 55 60
 Glu Asp Lys Phe Val Ser Phe Cys Tyr Gln Glu Ala Thr Val Thr Cys
 65 70 75 80
 Gly Ser Phe Asn Glu Ile Val Gly Cys Cys Tyr Gly Tyr Gln Met Cys
 85 90 95
 Met Ile Arg Val Val Lys Pro Asn Ser Leu Ser Gly Ala His Glu Ala
 100 105 110
 Cys Lys Thr Val Ser Cys Gly Asn Pro Cys Ala

115 120

<210> 216
 <211> 86
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(86)
 <223> Xaa at residues 11, 19, 28, 38, 48 and 74 is Glu or gamma-carboxy
 -Glu; Xaa at residues 3, 66 and 84 is Pro or hydroxy-Pro; Xaa at
 residues 24, 26, 54 and 56 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 216
 Ser Gly Xaa Ala Asp Cys Cys Arg Met Lys Xaa Cys Cys Thr Asp Arg
 1 5 10 15
 Val Asn Xaa Cys Leu Gln Arg Xaa Ser Gly Arg Xaa Asp Lys Phe Val
 20 25 30
 Ser Phe Cys Xaa Gln Xaa Ala Thr Val Thr Cys Gly Ser Phe Asn Xaa
 35 40 45
 Ile Val Gly Cys Cys Xaa Gly Xaa Gln Met Cys Met Ile Arg Val Val
 50 55 60
 Lys Xaa Asn Ser Leu Ser Gly Ala His Xaa Ala Cys Lys Thr Val Ser
 65 70 75 80
 Cys Gly Asn Xaa Cys Ala
 85

<210> 217
 <211> 14
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residues 1 and 3 is Trp (D or L) or bromo-Trp (D or L)

<400> 217
 Xaa Ser Xaa Arg Met Gly Asn Gly Asp Arg Arg Ser Asp Gln
 1 5 10

<210> 218
 <211> 343
 <212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (1)..(276)

<400> 218
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttg acc
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr

1	5	10	15	
ctg gca tcc agc cag cag gag gga gat gtc cag gca agg aaa aca agc				96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser	20	25	30	
ctg aag agc gac ttc tat cgt gct ctg aga ccg tat gac aga cag tgc				144
Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys	35	40	45	
act ttt gtc aac aat tgt caa cag aac ggt gcg tgt aac ggt gat tgc				192
Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys	50	55	60	
tct tgc ggg gac cag att tgt aaa tgc ggt tat aga atc agt cct ggg				240
Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly	65	70	75	80
agg tca gga tgc gcg tgt act tgt aga aat gcc aaa tgaatcactt				286
Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys	85	90		
aactcgttga aagattttta aaaatccaga gctatatgtt cgagaaaaaac cgaagac				343
<210>	219			
<211>	92			
<212>	PRT			
<213>	Conus striolatus			
<400>	219			
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr				
1	5	10	15	
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser	20	25	30	
Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys	35	40	45	
Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys	50	55	60	
Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly	65	70	75	80
Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys	85	90		
<210>	220			
<211>	46			
<212>	PRT			
<213>	Conus striolatus			
<220>				
<221>	PEPTIDE			
<222>	(1)..(46)			
<223>	Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 33 is Pro or hydroxy-Pro; Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr			

<400> 220

Xaa Cys Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly
 1 5 10 15

Asp Cys Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Xaa Arg Ile Ser
 20 25 30

Xaa Gly Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 35 40 45

<210> 221

<211> 398

<212> DNA

<213> *Conus tessulatus*

<220>

<221> CDS

<222> (7)..(240)

<400> 221

ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
 1 5 10

acg gcc tgt caa ttc att ata gct gat ttc tcc aga gat aag cgg gta 96
 Thr Ala Cys Gln Phe Ile Ile Ala Asp Phe Ser Arg Asp Lys Arg Val
 15 20 25 30

cat cgt gca gag agg ttg aga gac ata atg cag aat ttc aga ggt acc 144
 His Arg Ala Glu Arg Leu Arg Asp Ile Met Gln Asn Phe Arg Gly Thr
 35 40 45

agg tcg tgc gcg gaa ttt ggt gaa gtt tgt agt tct acc gct tgc tgc 192
 Arg Ser Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys
 50 55 60

cct gat ttg gat tgc gtt gag gcc tat tca ccc atc tgt ctc tgg gaa 240
 Pro Asp Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu
 65 70 75

tagtctggca tctgatattt cccgtctgtg ctctacctac ttctgccgga ttcatccata 300

cctatgtgtg gccatgaacc actcagtacc tacacctctg gtggcttctt agggacgtat 360

atcaaaataa aaccacattg caaaaaaaaaa aaaaaaaaaa 398

<210> 222

<211> 78

<212> PRT

<213> *Conus tessulatus*

<400> 222

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Phe Ile Ile Ala Asp Phe Ser Arg Asp Lys Arg Val His Arg
 20 25 30

Ala Glu Arg Leu Arg Asp Ile Met Gln Asn Phe Arg Gly Thr Arg Ser
 35 40 45

Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys Pro Asp
 50 55 60

Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu
 65 70 75

<210> 223
 <211> 31
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 4, 7 and 22 is Glu or gamma-carboxy-Glu; Xaa at r
 esidues 16 and 26 is Pro or hydroxy-Pro; Xaa at residue 30 is Trp
 (D or L) or bromo-Trp (D or L); Xaa at residue 24 is Tyr, 125I-T
 yr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 223
 Ser Cys Ala Xaa Phe Gly Xaa Val Cys Ser Ser Thr Ala Cys Cys Xaa
 1 5 10 15

Asp Leu Asp Cys Val Xaa Ala Xaa Ser Xaa Ile Cys Leu Xaa Xaa
 20 25 30

<210> 224
 <211> 273
 <212> DNA
 <213> Conus textile

<400> 224
 cgattgcagg ggttacgatg cgccgtgtag ctctggcgcg ccatgttgtg attggtggac 60
 atgttcagca cgaaccaacc gctgttttta ggctgaccac aagccatccg acatcaccac 120
 tctcctcttc agaggcttca aggccttttg ttctcctttt gaagaatcctt tacgagttaa 180
 caaacaagta gaatagcacg tttttccccc ttgaaaaat caataatgga ggttaaacaa 240
 aactgtcttc ttcaataaag attttatcat aat 273

<210> 225
 <211> 50
 <212> PRT
 <213> Conus textile

<400> 225
 Ile Gln Gly Gly Asp Glu Arg Gln Lys Ala Lys Ile Asn Phe Leu
 1 5 10 15

Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser
 20 25 30

Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser Ala Arg Thr Asn Arg
 35 40 45

Cys Phe
 50

<210> 226
 <211> 29
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residues 8 and 14 is Pro or hydroxy-Pro; Xaa at residues 1
 8 and 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-p
 hospho-Tyr

<400> 226
 Asp Cys Arg Gly Xaa Asp Ala Xaa Cys Ser Ser Gly Ala Xaa Cys Cys
 1 5 10 15
 Asp Xaa Xaa Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe
 20 25

<210> 227
 <211> 23
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residues 3,
 11, 12, 22 and 23 is Pro or hydroxy-Pro; Xaa at residues 4, 5 an
 d 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
 r O-phospho-Tyr

<400> 227
 Asn Cys Xaa Xaa Cys Val Val Xaa Cys Cys Xaa Xaa Ala Xaa Cys Xaa
 1 5 10 15
 Ala Ser Gly Cys Arg Xaa Xaa
 20

<210> 228
 <211> 205
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (1)..(186)

<400> 228
 atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg 96
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac 144

Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
35 40 45

aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt 186
Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
50 55 60

taaccagcat gaaggatcc 205

<210> 229
<211> 62
<212> PRT
<213> Conus textile

<400> 229
Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
20 25 30

Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
35 40 45

Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
50 55 60

<210> 230
<211> 12
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or
hydroxy-Pro; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di
-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 230
Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys
1 5 10

<210> 231
<211> 115
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (2)..(94)

<400> 231
g tta tgg agc gat tgc tat agt tgg tta gga tca tgt att gcg ccc tcg 49
Leu Trp Ser Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser
1 5 10 15

cag tgt tgt tct gag gtt tgt gat tat tac tgc cgc cta tgg cga 94
Gln Cys Cys Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg
20 25 30

tgaactcgga ccacaagcca t

115

<210> 232
 <211> 31
 <212> PRT
 <213> Conus textile

<400> 232
 Leu Trp Ser Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser
 1 5 10 15

Gln Cys Cys Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg
 20 25 30

<210> 233
 <211> 28
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 18 is Glu or gamma-carboxy-Glu; Xaa at residue 13
 is Pro or hydroxy-Pro; Xaa at residues 5 and 27 is Trp (D or L) o
 r bromo-Trp (D or L); Xaa at residue 3, 22 and 23 is Tyr, 125I-Ty
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 233
 Asp Cys Xaa Ser Xaa Leu Gly Ser Cys Ile Ala Xaa Ser Gln Cys Cys
 1 5 10 15

Ser Xaa Val Cys Asp Xaa Xaa Cys Arg Leu Xaa Arg
 20 25

<210> 234
 <211> 279
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (7)..(126)

<400> 234
 agctga cga atg aaa aat tcc gag aat gtc aag ctc agc aag aga aaa 48
 Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys
 1 5 10

tgt gtg gaa caa tgg aaa tac tgc acc cga gag tcc tta tgt tgc gcg 96
 Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala
 15 20 25 30

ggg ttg tgt ttg ttt agt ttc tgc att cta taacgcta ctagagtcgt 146
 Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu
 35 40

atattccgtc taagctccac ctggcactgt ctggtatggt cctgccagtg actggtctca 206

taccgcttag actctgggtcc gtcttctctg caaccacagg agaacgtgca ttattacaat 266

aaacgcatac tgc

279

<210> 235
 <211> 40
 <212> PRT
 <213> Conus textile

<400> 235
 Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys Cys Val
 1 5 10 15
 Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala Gly Leu
 20 25 30
 Cys Leu Phe Ser Phe Cys Ile Leu
 35 40

<210> 236
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 4 and 12 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 236
 Lys Cys Val Xaa Gln Xaa Lys Xaa Cys Thr Arg Xaa Ser Leu Cys Cys
 1 5 10 15
 Ala Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu
 20 25

<210> 237
 <211> 510
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (223)..(471)

<400> 237
 cagagccgct ctggtgtgca gacctgtctc cagccctccg tctccctgat cggtggttct 60
 gcctgcatag ctgtcttctc cacgaagctt tccacaggta taaataacgc ttcagtctcc 120
 cgtcctgtat tgggccgccc ttacaagcca gaccgataca gccagggtcca gtctactttg 180
 cgagtgaagt aaaagctcca gcattctacc agcatcacca ga atg aag gtg agc 234
 Met Lys Val Ser
 1
 agc gtg ctg atc gtg gct acg ctg aca ctg acc gca ggc cag ctg gtt 282
 Ser Val Leu Ile Val Ala Thr Leu Thr Leu Thr Ala Gly Gln Leu Val

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5              10              15              20
agt gct tct tcc cat tac tca aaa gat gtc cag att ctt cct tct gtg      330
Ser Ala Ser Ser His Tyr Ser Lys Asp Val Gln Ile Leu Pro Ser Val
              25              30              35

aga tca gct gac gaa gtg gaa aat tcc gag aat gtc agg ctc agc aag      378
Arg Ser Ala Asp Glu Val Glu Asn Ser Glu Asn Val Arg Leu Ser Lys
              40              45              50

aga aga tgt gtg gaa caa tgg gaa gtc tgc ggc ata atc ttg ttc tcc      426
Arg Arg Cys Val Glu Gln Trp Glu Val Cys Gly Ile Ile Leu Phe Ser
              55              60              65

tca tca tgt tgc ggg cag ttg tgt ttg ttt ggt ttc tgc gtt cta      471
Ser Ser Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu
              70              75              80

taacgctaata ccagagtcgt atattccgtc taagctcca      510

<210> 238
<211> 83
<212> PRT
<213> Conus textile

<400> 238
Met Lys Val Ser Ser Val Leu Ile Val Ala Thr Leu Thr Leu Thr Ala
1              5              10              15

Gly Gln Leu Val Ser Ala Ser Ser His Tyr Ser Lys Asp Val Gln Ile
              20              25              30

Leu Pro Ser Val Arg Ser Ala Asp Glu Val Glu Asn Ser Glu Asn Val
              35              40              45

Arg Leu Ser Lys Arg Arg Cys Val Glu Gln Trp Glu Val Cys Gly Ile
50              55              60

Ile Leu Phe Ser Ser Ser Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe
65              70              75              80

Cys Val Leu

<210> 239
<211> 29
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(29)
<223> Xaa at residues 3 and 6 is Glu or gamma-carboxy-Glu; Xaa at resid
ue 5 is Trp (D or L) or bromo-Trp (D or L)

<400> 239
Cys Val Xaa Gln Xaa Xaa Val Cys Gly Ile Ile Leu Phe Ser Ser Ser
1              5              10              15

Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu
20              25

```

<210> 240
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 9 and 13 is Glu or gamma-carboxy-Glu; Xaa at residues 4, 7 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 240

Cys Gly Gly Xaa Ser Thr Xaa Cys Xaa Val Asp Ser Xaa Cys Cys Ser
 1 5 10 15

Asp Asn Cys Val Arg Ser Xaa Cys Thr Leu Phe
 20 25

<210> 241
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

<400> 241

Gly Cys Asn Asn Ser Cys Gln Xaa His Ser Asp Cys Xaa Ser His Cys
 1 5 10 15

Ile Cys Thr Ser Arg Gly Cys Gly Ala Val Asn
 20 25

<210> 242
 <211> 373
 <212> DNA
 <213> Conus tulipa

<220>
 <221> CDS
 <222> (22)..(258)

<400> 242

caggattgaa caaaattcag g atg tca gga ttg gga atc atg gtg cta acc 51
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ctt cta ctt ctt gtg tcc atg gca acc agt cat cgt tat gca aga gaa 99
 Leu Leu Leu Leu Val Ser Met Ala Thr Ser His Arg Tyr Ala Arg Glu
 15 20 25

aag cag gcg acg cga agg gac gca gtc aac gtc aga cgg aga agc aga 147
 Lys Gln Ala Thr Arg Arg Asp Ala Val Asn Val Arg Arg Arg Ser Arg
 30 35 40

cca aaa aca aag gag tgc gaa agg tac tgt gag ctg gag gaa aag cac 195
 Pro Lys Thr Lys Glu Cys Glu Arg Tyr Cys Glu Leu Glu Glu Lys His
 45 50 55

tgc tgc tgc ata aga agt aac gga ccc aaa tgt tcc aga ata tgc ata 243
 Cys Cys Cys Ile Arg Ser Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile
 60 65 70

ttc aaa ttt tgg tgt tagttttctg tacactgtcc attcattatc ttatcagtac 298
 Phe Lys Phe Trp Cys
 75

aagtgtaaac gagacatgtc agaaagtcga aggttgtgcg taatttgata agcattgttt 358

actgggacga acgga 373

<210> 243

<211> 79

<212> PRT

<213> Conus tulipa

<400> 243

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser
 1 5 10 15

Met Ala Thr Ser His Arg Tyr Ala Arg Glu Lys Gln Ala Thr Arg Arg
 20 25 30

Asp Ala Val Asn Val Arg Arg Arg Ser Arg Pro Lys Thr Lys Glu Cys
 35 40 45

Glu Arg Tyr Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser
 50 55 60

Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile Phe Lys Phe Trp Cys
 65 70 75

<210> 244

<211> 37

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
 Xaa at residues 1 and 25 is Pro or hydroxy-Pro; Xaa at residue 36
 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
 sulpho-Tyr or O-phospho-Tyr

<400> 244

Xaa Lys Thr Lys Xaa Cys Xaa Arg Xaa Cys Xaa Leu Xaa Xaa Lys His
 1 5 10 15

Cys Cys Cys Ile Arg Ser Asn Gly Xaa Lys Cys Ser Arg Ile Cys Ile

	20	25	30	
Phe Lys Phe Xaa Cys				
	35			
<210>	245			
<211>	381			
<212>	DNA			
<213>	Conus tulipa			
<220>				
<221>	CDS			
<222>	(22) .. (267)			
<400>	245			
caggattgaa caaaattcag g atg tca gga ttg gga atc atg gtg cta acc				51
		Met Ser Gly Leu Gly Ile Met Val Leu Thr		
		1 5 10		
ctt ctc ctt ctt gtg cta atg aca acc agt cat cag gat gca gga gag				99
Leu Leu Leu Leu Val Leu Met Thr Thr Ser His Gln Asp Ala Gly Glu				
	15	20	25	
aag cag gcg atg caa agg gac gca aag aac ttc agt cgg aga aga tta				147
Lys Gln Ala Met Gln Arg Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu				
	30	35	40	
gtc att cgg aga cca aaa aca agg gag tgc gaa atg cag tgt gag cag				195
Val Ile Arg Arg Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln				
	45	50	55	
gag gag aaa cac tgc tgc cgc gta aga gat ggt acg ggc caa tgt gcc				243
Glu Glu Lys His Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala				
	60	65	70	
cct aag tgc ttg gga att aac tgg tagtttctgt acactgtctc attcattatc				297
Pro Lys Cys Leu Gly Ile Asn Trp				
	75	80		
ttatcagttac acgtgtaacg agacatgtca gaaagtcgaa ggtagtgcgt aatttgataa				357
gcattgttta ctgggacgaa cgga				381
<210>	246			
<211>	82			
<212>	PRT			
<213>	Conus tulipa			
<400>	246			
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Leu				
	1	5	10	15
Met Thr Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Met Gln Arg				
	20	25	30	
Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu Val Ile Arg Arg Pro Lys				
	35	40	45	
Thr Arg Glu Cys Glu Met Gln Cys Glu Gln Glu Glu Lys His Cys Cys				
	50	55	60	

Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Pro Lys Cys Leu Gly Ile
 65 70 75 80

Asn Trp

<210> 247

<211> 36

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
 Xaa at residues 1 and 29 is Pro or hydroxy-Pro; Xaa at residue 36
 is Trp (D or L) or bromo-Trp (D or L)

<400> 247

Xaa Lys Thr Arg Xaa Cys Xaa Met Gln Cys Xaa Gln Xaa Xaa Lys His
 1 5 10 15

Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Xaa Lys Cys Leu
 20 25 30

Gly Ile Asn Xaa
 35

<210> 248

<211> 363

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (1)..(264)

<400> 248

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30

ctg aag agc gac ttc tat cgt gct ctg cca agg ttt ggc cca ata tgc 144
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Pro Arg Phe Gly Pro Ile Cys
 35 40 45

act tgt ttt aaa agc cag aac tgt cgg ggt tct tgt gaa tgc atg tca 192
 Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser Cys Glu Cys Met Ser
 50 55 60

cct ccc ggt tgt tac tgc agt aac aat ggc att cgt gaa cga gga tgc 240
 Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys
 65 70 75 80

tcg tgt aca tgt cca ggg act ggt tgaatgattt gaaaaattca gagcaatatg 294

Ser Cys Thr Cys Pro Gly Thr Gly
85

ttgcagaaaa accgaagacc gagacttctc acaataaatc cataaagaca ttaaaaaaaaa 354

aaaaaaaaa 363

<210> 249

<211> 88

<212> PRT

<213> Conus tulipa

<400> 249

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Pro Arg Phe Gly Pro Ile Cys
35 40 45

Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser Cys Glu Cys Met Ser
50 55 60

Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys
65 70 75 80

Ser Cys Thr Cys Pro Gly Thr Gly
85

<210> 250

<211> 44

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(44)

<223> Xaa at residues 18 and 34 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 22, 23 and 42 is Pro or hydroxy-Pro; Xaa at residue 26 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 250

Phe Gly Xaa Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser
1 5 10 15

Cys Xaa Cys Met Ser Xaa Xaa Gly Cys Xaa Cys Ser Asn Asn Gly Ile
20 25 30

Arg Xaa Arg Gly Cys Ser Cys Thr Cys Xaa Gly Thr
35 40

<210> 251

<211> 383

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (1)..(276)

<400> 251

atg	atg	tcg	aaa	atg	gga	gct	atg	ttt	gtc	ctt	ttg	ctt	ctt	ttc	acc	48
Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Thr	
1				5					10					15		

ctg	gca	tcc	agc	cag	cag	gaa	gga	gat	gtc	cag	gca	agg	aaa	aca	cgc	96
Leu	Ala	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	Arg	
			20					25					30			

ctg	aag	agc	gac	ttc	tat	cgt	act	ctg	gca	ata	tct	gac	aga	gga	tgc	144
Leu	Lys	Ser	Asp	Phe	Tyr	Arg	Thr	Leu	Ala	Ile	Ser	Asp	Arg	Gly	Cys	
		35					40					45				

act	ggc	aac	tgt	gat	tgg	acg	tgt	agc	ggg	gat	tgc	agc	tgc	cag	ggc	192
Thr	Gly	Asn	Cys	Asp	Trp	Thr	Cys	Ser	Gly	Asp	Cys	Ser	Cys	Gln	Gly	
	50					55					60					

aca	tct	gac	tcg	tgt	cac	tgc	att	cca	cca	aaa	tca	ata	ggc	aac	aga	240
Thr	Ser	Asp	Ser	Cys	His	Cys	Ile	Pro	Pro	Lys	Ser	Ile	Gly	Asn	Arg	
65					70					75					80	

tgc	cgg	tgt	cag	tgt	aaa	aga	aaa	atc	gaa	att	gac	tgattctttt				286
Cys	Arg	Cys	Gln	Cys	Lys	Arg	Lys	Ile	Glu	Ile	Asp					
					85				90							

aactcgttga	acgattttaa	aatcagacca	atatgtaggc	agaaaaccga	agactctgag	346
------------	------------	------------	------------	------------	------------	-----

actctcgtaa	taatcgtaag	caaaaaaaaa	aaaaaaaa	383
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<210> 252

<211> 92

<212> PRT

<213> Conus tulipa

<400> 252

Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Thr
1				5					10					15	

Leu	Ala	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	Arg
			20					25					30		

Leu	Lys	Ser	Asp	Phe	Tyr	Arg	Thr	Leu	Ala	Ile	Ser	Asp	Arg	Gly	Cys
		35					40					45			

Thr	Gly	Asn	Cys	Asp	Trp	Thr	Cys	Ser	Gly	Asp	Cys	Ser	Cys	Gln	Gly
	50					55					60				

Thr	Ser	Asp	Ser	Cys	His	Cys	Ile	Pro	Pro	Lys	Ser	Ile	Gly	Asn	Arg
65					70					75					80

Cys	Arg	Cys	Gln	Cys	Lys	Arg	Lys	Ile	Glu	Ile	Asp				
				85					90						

<210> 253

<211> 46

<212> PRT

<213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(46)
 <223> Xaa at residue 44 is Glu or gamma-carboxy-Glu; Xaa at residues 27 and 28 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 253
 Gly Cys Thr Gly Asn Cys Asp Xaa Thr Cys Ser Gly Asp Cys Ser Cys
 1 5 10 15
 Gln Gly Thr Ser Asp Ser Cys His Cys Ile Xaa Xaa Lys Ser Ile Gly
 20 25 30
 Asn Arg Cys Arg Cys Gln Cys Lys Arg Lys Ile Xaa Ile Asp
 35 40 45

<210> 254
 <211> 404
 <212> DNA
 <213> *Conus virgo*

<220>
 <221> CDS
 <222> (7)..(243)

<400> 254
 ggatcc atg aaa ctg acg tgt gtg gtg atc atc act gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu
 1 5 10
 acg gcc agt cag ctc att aca gct gat tac tcc aga gat cag cgg cag 96
 Thr Ala Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln
 15 20 25 30
 tac cgt gca gtg agg ttg gga gat gaa atg cgg aat ttc aaa ggt gcc 144
 Tyr Arg Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala
 35 40 45
 agg gac tgc ggg gga caa ggt gaa ggt tgt tat act caa cct tgc tgc 192
 Arg Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys
 50 55 60
 cct ggt ctg cgg tgc cgt ggc ggc ggt act gga gga ggc gta tgc cag 240
 Pro Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Val Cys Gln
 65 70 75
 ctg tagtaatagt ttggcatctg atatttcccc tctgtgctcc accctctttt 293
 Leu
 gcctgattca tccttaccta tgtgtggtca tgaaccactc agtagctaca cctctggtgg 353
 attcagagaa cgtatatcaa aataaaacca cattgcaata aaaaaaaaaa a 404

<210> 255
 <211> 79
 <212> PRT
 <213> *Conus virgo*

<400> 255

Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu Thr Ala
1 5 10 15

Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln Tyr Arg
20 25 30

Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala Arg Asp
35 40 45

Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro Gly
50 55 60

Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu
65 70 75

<210> 256

<211> 32

<212> PRT

<213> *Conus virgo*

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residues 13
and 16 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 256

Asp Cys Gly Gly Gln Gly Xaa Gly Cys Xaa Thr Gln Xaa Cys Cys Xaa
1 5 10 15

Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu
20 25 30

<210> 257

<211> 285

<212> DNA

<213> *Conus radiatus*

<220>

<221> CDS

<222> (4)..(225)

<400> 257

atc atg cag aaa ctg aca atc ctg ctt ctt gtt gct gct ata ctg atg 48
Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met
1 5 10 15

tgc acc cag gtc ctg att caa ggt ggt gga gaa aaa cgc caa aaa gtc 96
Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val
20 25 30

aac att ttt tca aaa aga aag aca gat gct gag acc tgg tgg gag ggc 144
Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly
35 40 45

gaa tgc tct aat tgg tta gga agt tgt tgc acg ccc tca aat tgc tgt 192
Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
50 55 60

ctc aag agt tgt aat ggg cac tgc aca ttg tgg tgatgaactc tgaccacaaa 245
 Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
 65 70

gccatccaac atcacgcgtc tcctcttcag agtcttcaag 285

<210> 258
 <211> 74
 <212> PRT
 <213> Conus radiatus

<400> 258
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met Ser
 1 5 10 15
 Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val Asn
 20 25 30
 Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly Glu
 35 40 45
 Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys Leu
 50 55 60
 Lys Ser Cys Asn Gly His Cys Thr Leu Trp
 65 70

<210> 259
 <211> 31
 <212> PRT
 <213> Conus radiatus
 <220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 3 and is Glu or gamma-carboxy-Glu; Xaa at residue
 16 is Pro or hydroxy-Pro; Xaa at residues 1, 2, 9 and 31 is Trp
 (D or L) or bromo-Trp (D or L)

<400> 259
 Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa
 1 5 10 15
 Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa
 20 25 30

<210> 260
 <211> 296
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (1)..(237)

<400> 260
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gta ctg atg 48
 Ile Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15

tcc acc cag gcc ctg att caa ggt ggt gga gga aaa cgc caa cag gca 96
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala
 20 25 30

aag agc aag tat ttt tcc gaa aga aag gca cct gct aag cgt tgg ttt 144
 Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe
 35 40 45

gga cac gaa gaa tgc act tat tgg ttg ggg cct tgt gag gtg gac gac 192
 Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp
 50 55 60

acg tgt tgt tct gcc agt tgt gag tcc aag ttc tgc ggg ttg tgg 237
 Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp
 65 70 75

tgatggacac tgaccacaag tcatactaca tcgccactct cctgttcaga gtcttcaag 296

<210> 261
 <211> 79
 <212> PRT
 <213> *Conus radiatus*

<400> 261
 Ile Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15

Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala
 20 25 30

Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe
 35 40 45

Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp
 50 55 60

Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp
 65 70 75

<210> 262
 <211> 33
 <212> PRT
 <213> *Conus radiatus*

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 5, 6, 15 and 26 is Glu or gamma-carboxy-Glu; Xaa
 at residue 13 is Pro or hydroxy-Pro; Xaa at residues 1, 10 and 33
 is Trp (D or L) or bromo-Trp (D or L);

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
 sulpho-Tyr or O-phospho-Tyr

<400> 262
 Xaa Phe Gly His Xaa Xaa Cys Thr Xaa Xaa Leu Gly Xaa Cys Xaa Val

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1              5              10              15
Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu
      20              25              30

Xaa

<210> 263
<211> 306
<212> DNA
<213> Conus wittigi

<220>
<221> CDS
<222> (7)..(231)

<400> 263
ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc ttg ctg ttc ctg      48
      Met Lys Leu Thr Cys Val Val Ile Ile Ala Leu Leu Phe Leu
        1              5              10

acg gcc tgt cag ctc att acg gct gat tac tcc aga gat gag cag tct      96
Thr Ala Cys Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Glu Gln Ser
15              20              25              30

ggc agt aca gtg cgg ttt cta gac aga cca cgg cgt ttt ggt tcg ttc      144
Gly Ser Thr Val Arg Phe Leu Asp Arg Pro Arg Arg Phe Gly Ser Phe
              35              40              45

ata ccg tgc gcc cgt tta ggt gaa cca tgt acc ata tgc tgc cgt cct      192
Ile Pro Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile Cys Cys Arg Pro
              50              55              60

ttg agg tgc cgt gaa agc gga aca ccc aca tgt caa gtg tgattgtctg      241
Leu Arg Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln Val
        65              70              75

gcatctgata tttccctct gtgccctacc ctcttttgcc tgagtcatcc atacctgtgc      301

tcgag      306

<210> 264
<211> 75
<212> PRT
<213> Conus wittigi

<400> 264
Met Lys Leu Thr Cys Val Val Ile Ile Ala Leu Leu Phe Leu Thr Ala
1              5              10              15

Cys Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Glu Gln Ser Gly Ser
20              25              30

Thr Val Arg Phe Leu Asp Arg Pro Arg Arg Phe Gly Ser Phe Ile Pro
35              40              45

Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile Cys Cys Arg Pro Leu Arg
50              55              60

Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln Val

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<212> PRT

<213> Conus regius

<400> 267

Met Lys Leu Thr Cys Val Val Ile Met Ala Ser Leu Phe Leu Ala Ala
 1 5 10 15

Cys Gln Phe Leu Thr Ala Gly Gly Asp Ser Arg Ser Lys Gln Arg Tyr
 20 25 30

Pro Asp Trp Arg Leu Gly Tyr Arg Lys Ser Lys Leu Met Ala Lys Lys
 35 40 45

Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys
 50 55 60

Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln
 65 70 75

<210> 268

<211> 30

<212> PRT

<213> Conus regius

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residues 4 and 22 is Glu or gamma-carboxy-Glu; Xaa at residue 29 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11 and 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 268

Thr Cys Leu Xaa His Asn Lys Leu Cys Xaa Xaa Asp Arg Asp Cys Cys
 1 5 10 15

Thr Ile Xaa Cys Asn Xaa Asn Lys Cys Gly Val Lys Xaa Gln
 20 25 30

<210> 269

<211> 285

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (1)..(225)

<400> 269

atc atg cag aaa ctg aca atc ctg ctt ctt gtt gct gct ata ctg atg 48
 Ile Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met
 1 5 10 15

tgc acc cag gtc ctg att caa ggt ggt gga gaa aaa cgc caa aaa gtc 96
 Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val
 20 25 30

aac att ttt tca aaa aga aag aca gat gct gag acc tgg tgg gag ggc 144
 Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly


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          35              40              45
gaa tgc tct aat tgg tta gga agt tgt tcg acg ccc tca aat tgc tgt      192
Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
    50              55              60

ctc aag agt tgt aat ggg cac tgc aca ttg tgg tgatgaactc tgaccacaaa      245
Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
    65              70              75

gccatccaac atcaccgctc tcctcttcag agtcttcaag      285

<210> 270
<211> 75
<212> PRT
<213> Conus radiatus

<400> 270
Ile Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met
1              5              10              15

Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val
    20              25              30

Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly
    35              40              45

Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
    50              55              60

Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
    65              70              75

<210> 271
<211> 31
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 3 and 5 is Glu or gamma-carboxy-Glu; Xaa at resid
ue 16 is Pro or hydroxy-Pro; Xaa at residues 1,2, 9 and 31 is Trp
(D or L) or bromo-Trp (D or L)

<400> 271
Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa
1              5              10              15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa
    20              25              30

<210> 272
<211> 296
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (4)..(237)

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<400> 272
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gta ctg atg 48
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
 1 5 10 15
 tcc acc cag gcc ctg att caa ggt ggt gga gga aaa cgc caa cag gca 96
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala
 20 25 30
 aag agc aag tat ttt tcc gaa aga aag gca cct gct aag cgt tgg ttt 144
 Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe
 35 40 45
 gga cac gaa gaa tgc act tat tgg ttg ggg cct tgt gag gtg gac gac 192
 Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp
 50 55 60
 acg tgt tgt tct gcc agt tgt gag tcc aag ttc tgc ggg ttg tgg 237
 Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp
 65 70 75
 tgatggacac tgaccacaag tcatactaca tcgccactct cctgttcaga gtcttcaag 296

<210> 273
 <211> 78
 <212> PRT
 <213> Conus radiatus

<400> 273
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala Lys
 20 25 30
 Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe Gly
 35 40 45
 His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp Thr
 50 55 60
 Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp
 65 70 75

<210> 274
 <211> 33
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 5, 6, 15 and 26 is Glu or gamma-carboxy-Glu; Xaa
 at residue 13 is Pro or hydroxy-Pro; Xaa at residues 1, 10 and 33
 is Trp (D or L) or bromo-Trp (D or L);

<220>
 <221> PEPTIDE
 <222> (1)..(33)

<223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 274

Xaa Phe Gly His Xaa Xaa Cys Thr Xaa Xaa Leu Gly Xaa Cys Xaa Val
1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu
20 25 30

Xaa

<210> 275

<211> 387

<212> DNA

<213> Conus spurius

<220>

<221> CDS

<222> (21)..(212)

<400> 275

ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg att cca tct gca cct agc act gat gcc cga ccg aag acc aaa 101
Leu Leu Ile Pro Ser Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys
15 20 25

gat gat gtg cgc ctg gca tct ttc cac ggt aag gca aag cga acc cta 149
Asp Asp Val Arg Leu Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu
30 35 40

caa ata cct agg ggg aat atc cac tgt tgc aca aaa tat cag ccg tgc 197
Gln Ile Pro Arg Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys
45 50 55

tgt tct tca cca tca taaagggaaa tgactttgat gagaccctg cgaactgtcc 252
Cys Ser Ser Pro Ser
60

ctggatgtga aatttggaac cgagactggt cctttcgcgc gtgttcgtgg aatttcgaat 312

ggtcgttaat aacacgctgc ctcttgcaaa ctacaatctc tctgtccttt atctgtggac 372

tggatgtcaa cactg 387

<210> 276

<211> 64

<212> PRT

<213> Conus spurius

<400> 276

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Pro Ser
1 5 10 15

Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Arg Leu
20 25 30

Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu Gln Ile Pro Arg Gly
 35 40 45

Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro Ser
 50 55 60

<210> 277

<211> 17

<212> PRT

<213> Conus spurius

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 11 and 16 is Pro or hydroxy-Pro; Xaa at residue 9
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
 phospho-Tyr

<400> 277

Gly Asn Ile His Cys Cys Thr Lys Xaa Gln Xaa Cys Cys Ser Ser Xaa
 1 5 10 15

Ser

<210> 278

<211> 206

<212> DNA

<213> Conus nobilis

<220>

<221> CDS

<222> (1)..(183)

<400> 278

atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

gca cca agc gtt gat gcc cga ccg aag acc aaa gat gat gtg ctc cgg 96
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg
 20 25 30

gca tct ttc cgc gat aat gca aag agt acc cta caa aga ctt tgg aac 144
 Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn
 35 40 45

aaa cgc atc tgc tgc ccc ata att ctt tgg tgc tgt ggt taaccagcat 193
 Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly
 50 55 60

gaagttccca gga 206

<210> 279

<211> 61

<212> PRT

<213> Conus nobilis

<400> 279

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg
20 25 30

Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn
35 40 45

Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly
50 55 60

<210> 280

<211> 10

<212> PRT

<213> Conus nobilis

<220>

<221> PEPTIDE

<222> (1)..(10)

<223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 280

Ile Cys Cys Xaa Ile Ile Leu Xaa Cys Cys
1 5 10

<210> 281

<211> 205

<212> DNA

<213> Conus betulinus

<220>

<221> CDS

<222> (1)..(183)

<220>

<221> misc_feature

<222> (1)..(205)

<223> n is unknown

<400> 281

atg cgc tgt ctc cca gtc ttc atc att ctt ctg gtg ctg att gca tct 48
Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Val Leu Ile Ala Ser
1 5 10 15

gca cct acc gtt gat gcc cga cca aag atc gaa gat gat gag tcc ctg 96
Ala Pro Thr Val Asp Ala Arg Pro Lys Ile Glu Asp Asp Glu Ser Leu
20 25 30

gca tct ttc cat gnt cat naa cca cca tna nng ntn can ctt ttg aac 144
Ala Ser Phe His Xaa His Xaa Pro Pro Xaa Xaa Xaa Thr Leu Leu Asn
35 40 45

aaa cgc aat tgc tgc cca gac tct cct ccg tgc tgt cat taaccagcat 193
Lys Arg Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His
50 55 60

gaagggttcag ga 205

<210> 282

<211> 61

<212> PRT

<213> Conus betulinus

<220>

<221> misc_feature

<222> (1)..(61)

<223> Xaa is unknown

<400> 282

Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Val Leu Ile Ala Ser
 1 5 10 15

Ala Pro Thr Val Asp Ala Arg Pro Lys Ile Glu Asp Asp Glu Ser Leu
 20 25 30

Ala Ser Phe His Xaa His Xaa Pro Pro Xaa Xaa Xaa Thr Leu Leu Asn
 35 40 45

Lys Arg Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His
 50 55 60

<210> 283

<211> 11

<212> PRT

<213> Conus betulinus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residues 4, 7 and 8 is Pro or hydroxy-Pro

<400> 283

Asn Cys Cys Xaa Asp Ser Xaa Xaa Cys Cys His
 1 5 10

<210> 284

<211> 569

<212> DNA

<213> Conus purpurascens

<400> 284

ggaattccaa atgatgtaat tactgactac atggatcatag tgtataccca ttgaaaaatt 60

tctatgacat ttcagttggt agatcatcca gttccacaga tggaaagaca gagagatagt 120

agcttgcaag tggcagcgtg ttgttaacga ccattcgaca ttccatgaac acgtgtgaaa 180

ggagcagtct gctttccaaa tctgacatcc agggacagtt tgcaggggtc tcatccaaag 240

tcatcttctt ttatcccaaa gtacagcacc gcatctgttt tggacagcaa ccgcgtttct 300

tccaaaatct ttgtagggtt ccttttgcat tatcgtggaa agatgccagg ggcatatcat 360

ctttggtctt cggatgagca tcaacgcaag gtgcagatgg aatcagcagc agaagaatga 420

cgaagactgg cagacagcgc attctgcttg tagtcagctt ccgaattcca agccgaattc 480

tgcagatata catcacactg gcggccgctc gagcatgcat ctagagggcc caattggccc 540
 tatagtgagt cgtatgacaa ttcactggc 569

<210> 285

<211> 63

<212> PRT
 <213> Conus purpurascens

<400> 285
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Pro Ser
 1 5 10 15
 Ala Pro Cys Val Asp Ala His Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30
 Ala Ser Phe His Asp Asn Ala Lys Gly Thr Leu Gln Arg Phe Trp Lys
 35 40 45
 Lys Arg Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu Gly
 50 55 60

<210> 286
 <211> 12
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 4 is Pro or hydroxy-Pro

<400> 286
 Gly Cys Cys Xaa Lys Gln Met Arg Cys Cys Thr Leu
 1 5 10

<210> 287
 <211> 221
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (21)..(206)

<400> 287
 ggaagctgac tacaagcaga atg cac tgt ctc cca gtc gtc gtc att ctt ctg 53
 Met His Cys Leu Pro Val Val Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct ggt gga cct agc gtt gat gcc cga ctg aag acc 101
 Leu Leu Thr Ala Ser Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr
 15 20 25

aaa gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt atc 149
 Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile
 30 35 40

cta caa aga ctt tgg aag cga ggc aac tgc tgt gaa ttt tgg gag ttt 197
 Leu Gln Arg Leu Trp Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe
 45 50 55

tgc tgt gat taaccagcat gaagg 221
 Cys Cys Asp
 60

<210> 288
 <211> 62
 <212> PRT
 <213> Conus ammiralis

<400> 288
 Met His Cys Leu Pro Val Val Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro
 20 25 30
 Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile Leu Gln Arg Leu Trp
 35 40 45
 Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp
 50 55 60

<210> 289
 <211> 12
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residues 5 and 8 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Trp (D or L) or bromo-Trp (D or L)

<400> 289
 Gly Asn Cys Cys Xaa Phe Xaa Xaa Phe Cys Cys Asp
 1 5 10

<210> 290
 <211> 209
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (21)..(194)

<400> 290
 ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10
 ctg ctg act gca tct gga cct agc gtt gat gcc caa ccg aag acc gaa 101
 Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu
 15 20 25
 gtt gat gtg ccc ctg tca tct ttc cgc gat aat gca aag cgt gcc cta 149
 Val Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu
 30 35 40
 caa aga ctt ccg cgt tgc tgt gaa tat tgg aag ttg tgc tgt ggt 194
 Gln Arg Leu Pro Arg Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly
 45 50 55
 taaccagcat gaagg 209

<210> 291
 <211> 58
 <212> PRT
 <213> Conus dalli

<400> 291
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu Val Asp Val Pro Leu
 20 25 30
 Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu Gln Arg Leu Pro Arg
 35 40 45
 Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly
 50 55

<210> 292
 <211> 9
 <212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is
 Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr, 125
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 292
 Cys Cys Xaa Xaa Xaa Lys Leu Cys Cys
 1 5

<210> 293
 <211> 218
 <212> DNA
 <213> Conus omaria

<220>
 <221> CDS
 <222> (21)..(203)

<400> 293
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10
 ctg cta act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa 101
 Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys
 15 20 25
 gat gat gtg ccc ctg gca tct ttc cgt gat aat gca aag agt acc cta 149
 Asp Asp Val Pro Leu Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
 30 35 40
 caa aga ctt cag gac aaa cgc gtt tgc tgt ggc tat aag ttt ttt tgc 197
 Gln Arg Leu Gln Asp Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys
 45 50 55
 tgt cgt taaccagcat gaagg 218

Cys Arg
60

<210> 294
<211> 61
<212> PRT
<213> Conus omaria

<400> 294
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15
Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu
20 25 30
Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
35 40 45
Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg
50 55 60

<210> 295
<211> 11
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(11)
<223> Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 295
Val Cys Cys Gly Xaa Lys Phe Phe Cys Cys Arg
1 5 10

<210> 296
<211> 212
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (21)..(197)

<400> 296
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10
ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa 101
Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys
15 20 25
gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta 149
Asp Asp Val Pro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu
30 35 40
caa cat tgg aac caa cgc tgc tgc ccc atg atc tat tgg tgc tgt agt 197
Gln His Trp Asn Gln Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser

```

45                               50                               55
taaccagcat gaagg                                                    212

<210> 297
<211> 59
<212> PRT
<213> Conus aulicus

<400> 297
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1          5          10          15

Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
          20          25          30

Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln
          35          40          45

Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
          50          55

<210> 298
<211> 10
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (1)..(10)
<223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp (
D or L) or bromo-Trp (D or L); Xaa at residue 6 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 298
Cys Cys Xaa Met Ile Xaa Xaa Cys Cys Ser
1          5          10

<210> 299
<211> 212
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (21)..(197)

<400> 299
ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg      53
          Met His Cys Leu Pro Val Phe Val Ile Leu Leu
          1          5          10

ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa      101
Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys
          15          20          25

gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta      149
Asp Asp ValPro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu
          30          35          40

```

caa cat tgg aac caa cgc tgc tgc ccc gag atc tat tgg tgc tgt agt 197
 Gln His Trp Asn Gln Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
 45 50 55

taaccagcat gaagg 212

<210> 300
 <211> 59
 <212> PRT
 <213> Conus aulicus

<400> 300
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln
 35 40 45

Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
 50 55

<210> 301
 <211> 10
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residue 3 is
 Pro or hydroxy-Pro; Xaa at residue 7 is Trp (D or L) or bromo-Tr
 p (D or L); Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 301
 Cys Cys Xaa Xaa Ile Xaa Xaa Cys Cys Ser
 1 5 10

<210> 302
 <211> 215
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (21)..(200)

<400> 302
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10

ctg ctg att gca tct gca cct agc gtt gat gcc caa ccg aag acc aaa 101
 Leu Leu Ile Ala Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys
 15 20 25

gat gat gtg tcc ctg gca tct ttg cac gat aat ata aag agt act cta 149

Asp	Asp	Val	Ser	Leu	Ala	Ser	Leu	His	Asp	Asn	Ile	Lys	Ser	Thr	Leu	
		30					35				40					
caa	aca	ctt	tg	aac	aaa	cgc	tgc	tgc	ccc	cct	gtg	att	tg	tgc	tgt	197
Gln	Thr	Leu	Trp	Asn	Lys	Arg	Cys	Cys	Pro	Pro	Val	Ile	Trp	Cys	Cys	
	45					50					55					

ggt taaccagcat aaagg 215
Gly
60

```
<210> 303
<211> 60
<212> PRT
<213> Conus ammiralis
```

<400> 303
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
1 5 10 15

Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Ser Leu
20 25 30

Ala Ser Leu His Asp Asn Ile Lys Ser Thr Leu Gln Thr Leu Trp Asn
35 40 45

Lys Arg Cys Cys Pro Pro Val Ile Trp Cys Cys Gly
50 55 60

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<210> 304
<211> 9
<212> PRT
<213> Conus ammiralis
```

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<220>
<221>  PEPTIDE
<222>  (1)..(9)
<223>  Xaa at residues 3 and 4 is Pro or hydroxy-Pro; Xaa at residue 7 is
      Trp (D or L) or bromo-Trp (D or L)
```

<400> 304
Cys Cys Xaa Xaa Val Ile Xaa Cys Cys
1 5

<210>	305
<211>	215
<212>	DNA
<213>	Conus aulicus

```
<220>
<221> CDS
<222> (21) .. (200)
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<400> 305
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ccg aag acc aaa 101
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Lys
15 20 25

gat gat gtg cct ctg tca tct ttc cgc gat aac gca aag agt atc cta 149
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Ile Leu
 30 35 40

caa aga cgt tgg aac aac tat tgc tgc acg aat gag ctt tgg tgc tgt 197
 Gln Arg Arg Trp Asn Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys
 45 50 55

ggt taaccagcat gaagg 215
 Gly
 60

<210> 306
 <211> 60
 <212> PRT
 <213> Conus aulicus

<400> 306
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Ile Leu Gln Arg Arg Trp Asn
 35 40 45

Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys Gly
 50 55 60

<210> 307
 <211> 13
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa at residues 1 and 11 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 307
 Xaa Asn Asn Xaa Cys Cys Thr Asn Xaa Leu Xaa Cys Cys
 1 5 10

<210> 308
 <211> 218
 <212> DNA
 <213> Conus dalli

<220>
 <221> CDS
 <222> (21)..(203)

<400> 308
 ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu

	1	5	10	
ctg ctg act gca tct gga cct agc gtt gat gcc cga ccg aag acc gaa				101
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu				
	15	20	25	
gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt acc cta				149
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu				
	30	35	40	
caa aga ctt ttg aag cca gtc aac tgc tgt cct att gat caa tct tgc				197
Gln Arg Leu Leu Lys Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys				
	45	50	55	
tgt tct taaccagcat gaagg				218
Cys Ser				
60				
<210> 309				
<211> 61				
<212> PRT				
<213> Conus dalli				
<400> 309				
Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser				
1	5	10	15	
Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu Asp Asp Val Pro Leu				
	20	25	30	
Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu Gln Arg Leu Leu Lys				
	35	40	45	
Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser				
	50	55	60	
<210> 310				
<211> 13				
<212> PRT				
<213> Conus dalli				
<220>				
<221> PEPTIDE				
<222> (1)..(13)				
<223> Xaa at residues 1 and 6 is Pro or hydroxy-Pro				
<400> 310				
Xaa Val Asn Cys Cys Xaa Ile Asp Gln Ser Cys Cys Ser				
1	5	10		
<210> 311				
<211> 239				
<212> DNA				
<213> Conus consors				
<220>				
<221> CDS				
<222> (7)..(228)				
<400> 311				

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc atc cct tca gat cgt gca tct gaa ggc agg aat gcc gta gtc 96
 Val Ser Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val
 15 20 25 30

cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144
 His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys
 35 40 45

ggc tat gat ccg atg aca ata tgc cct cct tgc atg tgc act cat tcc 192
 Gly Tyr Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser
 50 55 60

tgt cca cca aaa aga aaa cca ggc cgc aga aac gac tgatgctcga g 239
 Cys Pro Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
 65 70

<210> 312
 <211> 74
 <212> PRT
 <213> Conus consors

<400> 312
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val His Glu
 20 25 30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
 35 40 45

Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro
 50 55 60

Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
 65 70

<210> 313
 <211> 36
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2,
 17, 22, 23, 31, 32 and 36 is Pro or hydroxy-Pro; Xaa at residue
 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 313
 Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp
 1 5 10 15

Xaa Met Thr Ile Cys Xaa Xaa Cys Met Cys Thr His Ser Cys Xaa Xaa
 20 25 30

Lys Arg Lys Xaa
35

<210> 314
<211> 272
<212> DNA
<213> Conus aurisiacus

<220>
<221> CDS
<222> (7)..(237)

<400> 314
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc atc cct tca gat cgt gca tct gat ggc agg aat gcc gca gtc 96
Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val
15 20 25 30

aac gag aga caa tct tgg ctg gtc cct tcg aca atc acg act tgc tgt 144
Asn Glu Arg Gln Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys
35 40 45

gga tat gat ccg ggg aca atg tgc cct cct tgc agg tgc aat aat acc 192
Gly Tyr Asp Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr
50 55 60

tgt aaa cca aaa aaa cca aaa cca gga aaa ggc cgc aga aac gac 237
Cys Lys Pro Lys Lys Pro Lys Pro Gly Lys Gly Arg Arg Asn Asp
65 70 75

tgatgctcca ggaccctctg aaccacgacc tcgag 272

<210> 315
<211> 77
<212> PRT
<213> Conus aurisiacus

<400> 315
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu
20 25 30

Arg Gln Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr
35 40 45

Asp Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys
50 55 60

Pro Lys Lys Pro Lys Pro Gly Lys Gly Arg Arg Asn Asp
65 70 75

<210> 316
<211> 39
<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(39)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 6, 17, 22, 23, 32, 35 and 37 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 316

Xaa Ser Xaa Leu Val Xaa Ser Thr Ile Thr Thr Cys Cys Gly Xaa Asp
1 5 10 15

Xaa Gly Thr Met Cys Xaa Xaa Cys Arg Cys Asn Asn Thr Cys Lys Xaa
20 25 30

Lys Lys Xaa Lys Xaa Gly Lys
35

<210> 317

<211> 266

<212> DNA

<213> Conus consors

<220>

<221> CDS

<222> (7)..(231)

<400> 317

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc atc cct tca gat cgt gca tct gat ggc agg aat gcc gta gtc 96
Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Val Val
15 20 25 30

cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144
His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys
35 40 45

ggc tat gat ccg atg aca tgg tgc cct tct tgc atg tgc act tat tcc 192
Gly Tyr Asp Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser
50 55 60

tgt ccc cac caa agg aaa aaa cca ggc cgc aga aac gac tgatgctcca 241
Cys Pro His Gln Arg Lys Lys Pro Gly Arg Arg Asn Asp
65 70 75

ggaccctctg aaccacgacc tcgag 266

<210> 318

<211> 75

<212> PRT

<213> Conus consors

<400> 318

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Val Val His Glu
20 25 30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
35 40 45

Asp Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro
50 55 60

His Gln Arg Lys Lys Pro Gly Arg Arg Asn Asp
65 70 75

<210> 319

<211> 37

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2, 17, 22, 31 and 37 is Pro or hydroxy-Pro; Xaa at residue 20 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 15 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 319

Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp
1 5 10 15

Xaa Met Thr Xaa Cys Xaa Ser Cys Met Cys Thr Xaa Ser Cys Xaa His
20 25 30

Gln Arg Lys Lys Xaa
35

<210> 320

<211> 260

<212> DNA

<213> Conus magus

<220>

<221> CDS

<222> (7)..(231)

<220>

<221> misc_feature

<222> (1)..(260)

<223> n is unknown

<400> 320

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc agt gtc
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ser Val
1 5 10

gtt tcc atc cct tca gat cgt gca tct gat ggc ggg aat gcc gta gtc 96
 Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Val Val
 15 20 25 30

cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144
 His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys
 35 40 45

ggc tat gat ccg atg aca ata tgc cct ccc tgc atg tgc act cat tcc 192
 Gly Tyr Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser
 50 55 60

tgt cca cca aaa gga aaa cca ggc cgc agg aac gac tga tgtccaggac 241
 Cys Pro Pro Lys Gly Lys Pro Gly Arg Arg Asn Asp
 65 70

ctctgaacca cgacncgag 260

<210> 321
 <211> 74
 <212> PRT
 <213> Conus magus

<400> 321
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ser Val Val Ser
 1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Val Val His Glu
 20 25 30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
 35 40 45

Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro
 50 55 60

Pro Lys Gly Lys Pro Gly Arg Arg Asn Asp
 65 70

<210> 322
 <211> 36
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2,
 17, 22, 23, 31, 32 and 36 is Pro or hydroxy-Pro; Xaa at residue 1
 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
 -phospho-Tyr

<400> 322
 Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp
 1 5 10 15

Xaa Met Thr Ile Cys Xaa Xaa Cys Met Cys Thr His Ser Cys Xaa Xaa
 20 25 30

Lys Gly Lys Xaa
35

<210> 323
<211> 251
<212> DNA
<213> Conus aurisiacus

<220>
<221> CDS
<222> (23)..(202)

<400> 323
gaattcgccc ttgaggatcc gt gtg gtt ctg ggt cca gaa cct gat ggc agg 52
Val Val Leu Gly Pro Glu Pro Asp Gly Arg
1 5 10

aat gcc gca gtc aac gag aga cag aaa tgg ctg gtc cat tcg aaa atc 100
Asn Ala Ala Val Asn Glu Arg Gln Lys Trp Leu Val His Ser Lys Ile
15 20 25

acg tat tgc tgt ggt tat aat aag atg gac atg tgc cct cct tgc atg 148
Thr Tyr Cys Cys Gly Tyr Asn Lys Met Asp Met Cys Pro Pro Cys Met
30 35 40

tgc act tat tcc tgt ccc ccc cta aaa aaa aaa aga cca ggc cgc aga 196
Cys Thr Tyr Ser Cys Pro Pro Leu Lys Lys Lys Arg Pro Gly Arg Arg
45 50 55

aac gac tgatgctcca ggaccctctg aaccacgacc tcgagcgaag ggcgaattc 251
Asn Asp
60

<210> 324
<211> 60
<212> PRT
<213> Conus aurisiacus

<400> 324
Val Val Leu Gly Pro Glu Pro Asp Gly Arg Asn Ala Ala Val Asn Glu
1 5 10 15

Arg Gln Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr
20 25 30

Asn Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro
35 40 45

Pro Leu Lys Lys Lys Arg Pro Gly Arg Arg Asn Asp
50 55 60

<210> 325
<211> 38
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(38)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 22, 23, 31,

32 and 38 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11, 15 and 28 is Tyr, 12 5I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 325

Xaa Lys Xaa Leu Val His Ser Lys Ile Thr Xaa Cys Cys Gly Xaa Asn
1 5 10 15

Lys Met Asp Met Cys Xaa Xaa Cys Met Cys Thr Xaa Ser Cys Xaa Xaa
20 25 30

Leu Lys Lys Lys Arg Xaa
35

<210> 326

<211> 212

<212> DNA

<213> *Conus aurisiacus*

<220>

<221> CDS

<222> (23)..(163)

<400> 326

gaattcgccc ttgaggatcc gt gtg gtt ctg ggt cca gca ttt gat ggc agg 52
Val Val Leu Gly Pro Ala Phe Asp Gly Arg
1 5 10

aat gcc gca gtc aac gag aga gcg cct tgg acg gtc gtt acg gcc acc 100
Asn Ala Ala Val Asn Glu Arg Ala Pro Trp Thr Val Val Thr Ala Thr
15 20 25

acg aat tgc tgc ggt att acc ggg cca ggc tgc ctt cct tgc cgt tgt 148
Thr Asn Cys Cys Gly Ile Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys
30 35 40

act caa aca tgt ggc tgatgctcca ggaccctctg aaccacgacc tcgagcgaag 203
Thr Gln Thr Cys Gly
45

ggcgaattc 212

<210> 327

<211> 47

<212> PRT

<213> *Conus aurisiacus*

<400> 327

Val Val Leu Gly Pro Ala Phe Asp Gly Arg Asn Ala Ala Val Asn Glu
1 5 10 15

Arg Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile
20 25 30

Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys Gly
35 40 45

<210> 328

<211> 29

<212> PRT

<213> *Conus aurisiacus*

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residues 2, 18 and 22 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L)

<400> 328

Ala Xaa Xaa Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr
1 5 10 15

Gly Xaa Gly Cys Leu Xaa Cys Arg Cys Thr Gln Thr Cys
20 25

<210> 329

<211> 218

<212> DNA

<213> *Conus marmoreus*

<220>

<221> CDS

<222> (21)..(203)

<400> 329

ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttg atc att ctt ctg 53
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu
1 5 10

ctg ctg act gca tct gca cct ggc gtt gtt gtc cta ccg aag acc gaa 101
Leu Leu Thr Ala Ser Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu
15 20 25

gat gat gtg ccc atg tca tct gtc tac ggt aat gga aag agt atc cta 149
Asp Asp Val Pro Met Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu
30 35 40

cga ggg att ctg agg aac ggt gtt tgc tgt ggc tat aag ttg tgc ctt 197
Arg Gly Ile Leu Arg Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu
45 50 55

cca tgt taaccagcat gaagg 218
Pro Cys
60

<210> 330

<211> 61

<212> PRT

<213> *Conus marmoreus*

<400> 330

Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met
20 25 30

Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg
35 40 45

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu Pro Cys
 50 55 60

<210> 331
 <211> 13
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 331
 Asn Gly Val Cys Cys Gly Xaa Lys Leu Cys Leu Xaa Cys
 1 5 10

<210> 332
 <211> 238
 <212> DNA
 <213> Conus pennaceus

<220>
 <221> CDS
 <222> (28)..(219)

<400> 332
 ggaattcgga agctgactac aagcaga atg cgc tgt ctc cca gtc ttc gtc att 54
 Met Arg Cys Leu Pro Val Phe Val Ile
 1 5

ctt ctg ctg ctg act gca tct gca cct agc gtt gat gcc aaa gtt cat 102
 Leu Leu Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Lys Val His
 10 15 20 25

ctg aag acc aaa ggt gat ggg ccc ctg tca tct ttc cga gat aat gca 150
 Leu Lys Thr Lys Gly Asp Gly Pro Leu Ser Ser Phe Arg Asp Asn Ala
 30 35 40

aag agt acc cta caa aga ctt cag gac aaa agc act tgc tgt ggc ttt 198
 Lys Ser Thr Leu Gln Arg Leu Gln Asp Lys Ser Thr Cys Cys Gly Phe
 45 50 55

aag atg tgt atc cct tgt agt taaccagcat gaaggatcc 238
 Lys Met Cys Ile Pro Cys Ser
 60

<210> 333
 <211> 64
 <212> PRT
 <213> Conus pennaceus

<400> 333
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser
 50 55 60

<210> 334

<211> 13

<212> PRT

<213> Conus pennaceus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 334

Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Ser
 1 5 10

<210> 335

<211> 231

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (27)..(212)

<400> 335

gaattcggaa gctgactaca agcaga atg cgt tgt ctc cca gtc ttc gtc att 53
 Met Arg Cys Leu Pro Val Phe Val Ile
 1 5

ctt ctg ctg ctg act gca tct gga cct agc gtt gat gcc cga ctg aag 101
 Leu Leu Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Leu Lys
 10 15 20 25

acc aaa gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt 149
 Thr Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser
 30 35 40

acc cta caa aga ctt cag gac aaa cgc ctt tgc tgt ggc ttt tgg atg 197
 Thr Leu Gln Arg Leu Gln Asp Lys Arg Leu Cys Cys Gly Phe Trp Met
 45 50 55

tgt att cct tgt aat taaccagcat gaaggatcc 231
 Cys Ile Pro Cys Asn
 60

<210> 336

<211> 62

<212> PRT

<213> Conus pennaceus

<400> 336

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
 35 40 45

Lys Arg Leu Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn
 50 55 60

<210> 337

<211> 12

<212> PRT

<213> Conus pennaceus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 6 is Trp
 (D or L) or bromo-Trp (D or L)

<400> 337

Leu Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Asn
 1 5 10

<210> 338

<211> 244

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (40)..(225)

<220>

<221> misc_feature

<222> (1)..(244)

<223> n is unknown

<400> 338

gaattctccc ttggaattct gaagctgact acaancaga atg cgt tgt ctc cca 54
 Met Arg Cys Leu Pro
 1 5

ctc ttc gtc att ctt ctg ctg ctg act gca tct gga cct act gtt gat 102
 Leu Phe Val Ile Leu Leu Leu Leu Thr Ala Ser Gly Pro Thr Val Asp
 10 15 20

gcc cga ctg aag acc aaa gat gat gtg ccc ctg tca tct ttc cga gat 150
 Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp
 25 30 35

aat gca aag agt acc cta caa aga ctt cag gac aaa agc act tgc tgt 198
 Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp Lys Ser Thr Cys Cys
 40 45 50

ggc ttt aag atg tgt att cct tgt ggt taaccagcat gaaggatcc 244
 Gly Phe Lys Met Cys Ile Pro Cys Gly
 55 60

<210> 339
 <211> 62
 <212> PRT
 <213> Conus pennaceus

<400> 339
 Met Arg Cys Leu Pro Leu Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Pro Thr Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
 35 40 45
 Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Gly
 50 55 60

<210> 340
 <211> 12
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 340
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys
 1 5 10

<210> 341
 <211> 250
 <212> DNA
 <213> Conus episcopatus

<220>
 <221> misc_feature
 <222> (1)..(250)
 <223> n is unknown

<400> 341
 gaattcgccc ttggaattcg gaagctgact acaagcagaa tgcgctgtct cccagtcttc 60
 gtcattcttc tgctgctgac tgcattctgga cctantgttg atgccaaagt tcatctgaag 120
 accaaaggtg atgggccct gtcattcttc cgagataatg caaagagtac cctacaaaga 180
 cttcaggaca aaagcacttg ctgtggctat aggatgtgtg ttccttgtgg ttaaccagca 240
 tgaaggatcc 250

<210> 342
 <211> 64
 <212> PRT
 <213> Conus episcopatus

<400> 342

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Gly Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
50 55 60

<210> 343

<211> 12

<212> PRT

<213> *Conus episcopatus*

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr
, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Tyr

<400> 343

Ser Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys
1 5 10

<210> 344

<211> 827

<212> DNA

<213> *Conus marmoreus*

<220>

<221> CDS

<222> (82)..(264)

<400> 344

ggcgaataca cctggcaggt actcaacgaa cttcaggaca cattcttttc acctggacac 60

tggaaactga caacaggcag a atg cgc tgt ctc cca gtc ttg atc att ctt 111
Met Arg Cys Leu Pro Val Leu Ile Ile Leu
1 5 10

ctg ctg ctg act gca tct gca cct ggc gtt gtt gtc cta ccg aag acc 159
Leu Leu Leu Thr Ala Ser Ala Pro Gly Val Val Val Leu Pro Lys Thr
15 20 25

gaa gat gat gtg ccc atg tca tct gtc tac ggt aat gga aag agt atc 207
Glu Asp Asp Val Pro Met Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile
30 35 40

cta cga gga att ctg agg aac ggt gtt tgc tgt ggc tat aag ttg tgc 255
Leu Arg Gly Ile Leu Arg Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys
45 50 55

cat cca tgt taaccagcat gaagggaaat gactttggat gagaccctg 304
His Pro Cys
60

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cgaactgtcc ctggatgtga aatttgga aa gacactgtt cctttcgac gtattcgtgg 364
aatttcgaat ggtcgtaaac aacacgtgc cacttgcagg ctactatctc tctgtccttt 424

catctgtgga aatggatgat ctaacaactg aaatatacaga aatttttcaa tggctataca 484
ctatgaccat gtagtcagta attatatcat ttggaccttt tgaaatatatt ttcaatatgt 544
aaagtttttg caccctggaa aggtcttttg gagttaaata ttttagtatg ttatgttttg 604
catacaagtt atagaatgct gtctttcttt ttgttccac atcaatgggtg ggggcagaaa 664
ttatttgttt tggccaatgt aattatgacc tgcatttagt gctatagtga ttgcattttc 724
agcgtggaat gtttaatctg caaacagaaa gtggttgatc gactaataaa gatttgcatg 784
gcacaaaaaa aaaaaaaaaa agtactctgc gttgttactc gag 827

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<210> 345

<211> 61

<212> PRT

<213> Conus marmoreus

<400> 345

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Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1           5           10           15

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Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met
20           25           30

```

```

Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg
35           40           45

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```

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys
50           55           60

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<210> 346

<211> 13

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 346

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Asn Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys
1           5           10

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<210> 347

<211> 12

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,

125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 347

Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys
1 5 10

<210> 348

<211> 202

<212> DNA

<213> Conus bandanus

<220>

<221> CDS

<222> (1)..(183)

<400> 348

atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96
Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
20 25 30

tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144
Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
35 40 45

aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193
Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
50 55 60

gaaggatcc 202

<210> 349

<211> 61

<212> PRT

<213> Conus bandanus

<400> 349

Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
20 25 30

Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
35 40 45

Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
50 55 60

<210> 350

<211> 11

<212> PRT

<213> Conus bandanus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 350

Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys
1 5 10

<210> 351

<211> 221

<212> DNA

<213> Conus aulicus

<220>

<221> CDS

<222> (21)..(206)

<400> 351

ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ctg aag acc aaa 101
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys
15 20 25

gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt acc cta 149
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
30 35 40

caa aga cat cag gac aaa agc gtt tgc tgt ggc tat aag ctg tgt ttt 197
Gln Arg His Gln Asp Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe
45 50 55

cct tgt ggt taaccagcat gaagg 221
Pro Cys Gly
60

<210> 352

<211> 62

<212> PRT

<213> Conus aulicus

<400> 352

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu
20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg His Gln Asp
35 40 45

Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe Pro Cys Gly
50 55 60

<210> 353

<211> 12

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
Tyr

<400> 353

Ser Val Cys Cys Gly Xaa Lys Leu Cys Phe Xaa Cys
1 5 10

<210> 354

<211> 312

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (3)..(50)

<220>

<221> misc_feature

<222> (1)..(312)

<223> n is unknown

<400> 354

ca gga tcc aat ggg gtt tgt tgt ggc tat agg atg tgt gtt cct tgt 47
Gly Ser Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
1 5 10 15

ggt taaccagcat gaagggaaat gactttggat gagaccctg cgaactgtcc 100
Gly

ctggatgtga gatttggaaa gcagactgtt cattttgcac gtgttcgtgg aatttcgaat 160

ggtcgttaac aacacgctgc cacttgcaag ctactatctc tctgtccttt tatctgtgga 220

actgtatgat ctaacaactg aaatatcata nanatttttc aatgggtatn cactatgcat 280

atgatcatgt agggttcaag ggggtcaagat nc 312

<210> 355

<211> 16

<212> PRT

<213> Conus textile

<400> 355

Gly Ser Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
1 5 10 15

<210> 356

<211> 13

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 356
 Asn Gly Val Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys
 1 5 10

<210> 357
 <211> 205
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (1)..(186)

<400> 357
 atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg 96
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac 144
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
 35 40 45
 aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt 186
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
 50 55 60
 taaccagcat gaaggatcc 205

<210> 358
 <211> 62
 <212> PRT
 <213> Conus textile

<400> 358
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
 35 40 45
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
 50 55 60

<210> 359
 <211> 12
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 359
 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys
 1 5 10

<210> 360
 <211> 221
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (21)..(206)

<400> 360
 agaagctgac tacaagcaga atg cac tac ctc cca gtc ttc gtc att ctt ctg 53
 Met His Tyr Leu Pro Val Phe Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc caa ctg aag acc aaa 101
 Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys
 15 20 25

gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt acc cta 149
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
 30 35 40

cga aga ctc cag tac aaa cag gct tgc tgt ggc ttt aag atg tgt gtt 197
 Arg Arg Leu Gln Tyr Lys Gln Ala Cys Cys Gly Phe Lys Met Cys Val
 45 50 55

cct tgt ggt taaccagcat gaagg 221
 Pro Cys Gly
 60

<210> 361
 <211> 62
 <212> PRT
 <213> Conus ammiralis

<400> 361
 Met His Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Arg Arg Leu Gln Tyr
 35 40 45

Lys Gln Ala Cys Cys Gly Phe Lys Met Cys Val Pro Cys Gly
 50 55 60

<210> 362
 <211> 12
 <212> PRT
 <213> *Conus ammiralis*

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or hydroxy-Pro

<400> 362
 Xaa Ala Cys Cys Gly Phe Lys Met Cys Val Xaa Cys
 1 5 10

<210> 363
 <211> 211
 <212> DNA
 <213> *Conus pennaceus*

<220>
 <221> CDS
 <222> (1)..(192)

<400> 363
 atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30
 ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45
 cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt cgt 192
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 50 55 60
 taaccagcat gaaggatcc 211

<210> 364
 <211> 64
 <212> PRT
 <213> *Conus pennaceus*

<400> 364
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 50 55 60

<210> 365
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 13 is Pro or hydroxy-Pro

<400> 365
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Arg
 1 5 10

<210> 366
 <211> 304
 <212> DNA
 <213> Conus pennaceus

<220>
 <221> CDS
 <222> (3)..(50)

<220>
 <221> misc_feature
 <222> (1)..(304)
 <223> n is unknown

<400> 366
 ca gga tcc aat ggg gtt tgt tgt ggc ttt tgg atg tgt att cct tgt 47
 Gly Ser Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys
 1 5 10 15

aat taaccagcat gaagggaaat gactttggat aagaccctg cgaactgtcc 100
 Asn

ttggatgtga gatttggaaa gcagactggt ccttttgcac gtgttcgtgg aatttcgaat 160

ggtcgttaac aacacgctgc cacttgcaag ctactatctc tctgtccttt catctgtgga 220

actgtatgat ctaacaactg aaatatcata gaaatttttc aatgggtata cactatgcat 280

atgaccatgt angggtcaac agnc 304

<210> 367
 <211> 16
 <212> PRT
 <213> Conus pennaceus

<400> 367
 Gly Ser Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn
 1 5 10 15

<210> 368
 <211> 14
 <212> PRT
 <213> Conus pennaceus

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<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp
      (D or L) or bromo-Trp (D or L)

<400> 368
Asn Gly Val Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Asn
1          5          10

<210> 369
<211> 218
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (21)..(203)

<400> 369
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg      53
                Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
                1          5          10

ctg ctg act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa      101
Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys
                15          20          25

gat gat gtg ccc ctg tca tct ttc cgt gat aat gca aag agt acc cta      149
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
                30          35          40

caa aga ctt cag gac aaa gac gtt tgc tgt tac gtt aga atg tgt cct      197
Gln Arg Leu Gln Asp Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro
                45          50          55

tgt cgt taaccagcat gaagg      218
Cys Arg
60

<210> 370
<211> 61
<212> PRT
<213> Conus omaria

<400> 370
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1          5          10          15

Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu
                20          25          30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
                35          40          45

Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro Cys Arg
                50          55          60

<210> 371

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<211> 12
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 371
 Asp Val Cys Cys Xaa Val Arg Met Cys Xaa Cys Arg
 1 5 10

<210> 372
 <211> 84
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(84)
 <223> Xaa at residues 27, 32, 38, 39 and 41 is Glu or gamma-carboxy-Glu
 ; Xaa at residues 2, 5, 17, 23, 43, 45 and 58 is Pro or hydroxy-P
 ro;Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 372
 His Xaa Thr Lys Xaa Cys Met Xaa Cys Ser Phe Gly Gln Cys Val Gly
 1 5 10 15

Xaa His Ile Cys Cys Gly Xaa Thr Gly Cys Xaa Met Gly Thr Ala Xaa
 20 25 30

Ala Asn Met Cys Ser Xaa Xaa Asp Xaa Asp Xaa Ile Xaa Cys Gln Val
 35 40 45

Phe Gly Ser Asp Cys Ala Leu Asn Asn Xaa Asp Asn Ile His Gly His
 50 55 60

Cys Val Ala Asp Gly Ile Cys Cys Val Asp Asp Thr Cys Thr Thr His
 65 70 75 80

Leu Gly Cys Leu

<210> 373
 <211> 218
 <212> DNA
 <213> Conus tessulatus

<220>
 <221> CDS
 <222> (7)..(174)

<400> 373
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ttc agt gca gat cgt gcc aac gtc aaa gcg tct gac ctg atc 96
 Val Ser Phe Ser Ala Asp Arg Ala Asn Val Lys Ala Ser Asp Leu Ile
 15 20 25 30

gcc cag gcc acc aga gac ggc tgt cca cca cat ccc gtt cct ggc atg 144
 Ala Gln Ala Thr Arg Asp Gly Cys Pro Pro His Pro Val Pro Gly Met
 35 40 45

cat aag tgc atg tgt act aat aca tgt ggt tgaagacgct gatgctccag 194
 His Lys Cys Met Cys Thr Asn Thr Cys Gly
 50 55

gaccctctga accacgacct cgag 218

<210> 374

<211> 56

<212> PRT

<213> Conus tessulatus

<400> 374

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Ser Ala Asp Arg Ala Asn Val Lys Ala Ser Asp Leu Ile Ala Gln
 20 25 30

Ala Thr Arg Asp Gly Cys Pro Pro His Pro Val Pro Gly Met His Lys
 35 40 45

Cys Met Cys Thr Asn Thr Cys Gly
 50 55

<210> 375

<211> 20

<212> PRT

<213> Conus tessulatus

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> Xaa at residues 4, 5, 7 and 9 is Pro or hydroxy-Pro

<400> 375

Asp Gly Cys Xaa Xaa His Xaa Val Xaa Gly Met His Lys Cys Met Cys
 1 5 10 15

Thr Asn Thr Cys
 20

<210> 376

<211> 536

<212> DNA

<213> Conus geographus

<220>

<221> CDS

<222> (400)..(510)

<220>

<221> misc_feature

<222> (1)..(536)

<223> n is unknown

<400> 376

anntagantn tgctgtanta nnggatcnta antantgnnt cganatgatn angagtgata 60

aatgannggt gcactnntan ttangntnnt angatnnnna tattatnnta nnnnntaana 120

natatnggt nngannaaga agantaaaag tanngnttng tgaaanaang annnnatggt 180

nnanntcata acnnnaatgt aaataatana cgnnccagtg tgaaannntn tcnnnnataa 240

aaattctntn tntnaangtn nntgtntgng tgtgtgtgtg tgtgtgtgtg tgtgngtgtg 300

tgngtgtgtg tgtgtgtgtg tgtgtgtgtg nggtgtgtgn tgtgngtgtg tgtgtgtgtg 360

tgtgtgtgtg tgtgtgtgtg tgtggttctg ggtccagca tct gat gnc agg gat 414
 Ser Asp Xaa Arg Asp
 1 5

gac aca gcc aaa gac gaa ggg tct nac atg gac aaa ttg gtc gag aaa 462

Asp Thr Ala Lys Asp Glu Gly Ser Xaa Met Asp Lys Leu Val Glu Lys
 10 15 20

aaa gaa tgt tgc cat cct gcc tgt ggc aaa cac tac agt tgt gga cgc 510

Lys Glu Cys Cys His Pro Ala Cys Gly Lys His Tyr Ser Cys Gly Arg
 25 30 35

tgatgctcca gggntgaag gancaa 536

<210> 377

<211> 37

<212> PRT

<213> Conus geographus

<220>

<221> misc_feature

<222> (1)..(37)

<223> Xaa is unknown

<400> 377

Ser Asp Xaa Arg Asp Asp Thr Ala Lys Asp Glu Gly Ser Xaa Met Asp
 1 5 10 15

Lys Leu Val Glu Lys Lys Glu Cys Cys His Pro Ala Cys Gly Lys His
 20 25 30

Tyr Ser Cys Gly Arg
 35

<210> 378

<211> 13

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is
 Pro or hydroxy-Pro; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iod
 o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 378

Xaa Cys Cys His Xaa Ala Cys Gly Lys His Xaa Ser Cys
 1 5 10

<210> 379

<211> 217

<212> DNA

<213> Conus geographus

<220>

<221> CDS

<222> (7)..(183)

<400> 379

ggatcc atg ttc acc gtg ttt ctg ttg gtg gtc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ttc cct tca gaa cgt gca tct gat ggc agg gat gac aca gcc 96
 Val Ser Phe Pro Ser Glu Arg Ala Ser Asp Gly Arg Asp Asp Thr Ala
 15 20 25 30

aaa gac gaa ggg tct gac atg gag aaa ttg gtc gag aaa aaa gaa tgt 144
 Lys Asp Glu Gly Ser Asp Met Glu Lys Leu Val Glu Lys Lys Glu Cys
 35 40 45

tgc aat cct gcc tgt ggc aga cac ttc agt tgt gga cgc tgatgctcca 193
 Cys Asn Pro Ala Cys Gly Arg His Phe Ser Cys Gly Arg
 50 55

ggaccctctg aaccacgact cgag 217

<210> 380

<211> 59

<212> PRT

<213> Conus geographus

<400> 380

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Pro Ser Glu Arg Ala Ser Asp Gly Arg Asp Asp Thr Ala Lys Asp
 20 25 30

Glu Gly Ser Asp Met Glu Lys Leu Val Glu Lys Lys Glu Cys Cys Asn
 35 40 45

Pro Ala Cys Gly Arg His Phe Ser Cys Gly Arg
 50 55

<210> 381

<211> 13

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is

Pro or hydroxy-Pro

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<400> 381
Xaa Cys Cys Asn Xaa Ala Cys Gly Arg His Phe Ser Cys
1           5           10

<210> 382
<211> 224
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (7)..(207)

<400> 382
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc      48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1           5           10

gtt tcc ttc act tca gat cgt gca tct gat ggc agg gat gac gaa gcc      96
Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala
15          20          25          30

aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aaa gga cgc gca      144
Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala
          35          40          45

tac tgt tgc cat cct gcc tgt ggc cca aac tat agt tgt ggc acc tca      192
Tyr Cys Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr Ser
          50          55          60

tgc tcc agg acc ctc tgaaccacga cctcgag      224
Cys Ser Arg Thr Leu
          65

<210> 383
<211> 67
<212> PRT
<213> Conus striatus

<400> 383
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1           5           10          15

Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp
          20          25          30

Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala Tyr Cys
          35          40          45

Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr Ser Cys Ser
          50          55          60

Arg Thr Leu
65

<210> 384
<211> 22
<212> PRT

```

<213> *Conus striatus*

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residues 6 and 10 is Pro or hydroxy-Pro; Xaa at residues 2 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 384

Ala Xaa Cys Cys His Xaa Ala Cys Gly Xaa Asn Xaa Ser Cys Gly Thr
1 5 10 15

Ser Cys Ser Arg Thr Leu
20

<210> 385

<211> 224

<212> DNA

<213> *Conus striatus*

<220>

<221> CDS

<222> (7)..(189)

<400> 385

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc ttc act tca gat cgt gca tct gat ggc agg gat gac gaa gcc 96
Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala
15 20 25 30

aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aaa gga cgc gca 144
Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala
35 40 45

tac tgt tgc cat cct gtc tgt ggc aaa aac ttt gat tgt gga cgc 189
Tyr Cys Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys Gly Arg
50 55 60

tgatgctcca ggaccctctg aaccacgacc tcgag 224

<210> 386

<211> 61

<212> PRT

<213> *Conus striatus*

<400> 386

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp
20 25 30

Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala Tyr Cys
35 40 45

Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys Gly Arg

```

50                               55                               60
<210> 387
<211> 14
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 2 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
yr

<400> 387
Ala Xaa Cys Cys His Xaa Val Cys Gly Lys Asn Phe Asp Cys
1          5          10

<210> 388
<211> 224
<212> DNA
<213> Conus rattus

<220>
<221> CDS
<222> (7)..(207)

<400> 388
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc          48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1          5          10

gtt tcc ttc cct tca gat cgt gca tct gat ggc agg gat gac gaa gcc          96
Val Ser Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala
15         20         25         30

aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aat gga cgc gga          144
Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Asn Gly Arg Gly
35         40         45

tgc tgt tgc aat cct gcc tgt ggc cca aac tat ggt tgt ggc acc tca          192
Cys Cys Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr Ser
50         55         60

tgc tcc agg acc ctc tgaaccacga cctcgag          224
Cys Ser Arg Thr Leu
65

<210> 389
<211> 67
<212> PRT
<213> Conus rattus

<400> 389
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10         15

Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp
20         25         30

```

Glu Arg Ser Asp Met His Glu Ser Asp Arg Asn Gly Arg Gly Cys Cys
 35 40 45

Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr Ser Cys Ser
 50 55 60

Arg Thr Leu
 65

<210> 390
 <211> 22
 <212> PRT
 <213> Conus rattus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residues 6 and 10 is Pro or hydroxy-Pro; XXaa at residue 1
 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
 -phospho-Tyr

<400> 390
 Gly Cys Cys Cys Asn Xaa Ala Cys Gly Xaa Asn Xaa Gly Cys Gly Thr
 1 5 10 15

Ser Cys Ser Arg Thr Leu
 20

<210> 391
 <211> 230
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (7)..(195)

<400> 391
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gat tcc ttc act cca gtt cgt act tct gtt ggc agg agt gct gca gcc 96
 Asp Ser Phe Thr Pro Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala
 15 20 25 30

aac gcg ttt gac cgg atc gct ctg acc gcc agg caa gat tat tgc tgt 144
 Asn Ala Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys
 35 40 45

acc att ccc agc tgt tgg gat cgc tat aaa gag aga tgt aga cac ata 192
 Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile
 50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc ttgag 230
 Arg

<210> 392
 <211> 63
 <212> PRT

<213> Conus arenatus

<400> 392

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Asp Ser
1 5 10 15

Phe Thr Pro Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala Asn Ala
20 25 30

Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys Thr Ile
35 40 45

Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile Arg
50 55 60

<210> 393

<211> 22

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at residue 11 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residues 3 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 393

Xaa Asp Xaa Cys Cys Thr Ile Xaa Ser Cys Xaa Asp Arg Xaa Lys Xaa
1 5 10 15

Arg Cys Arg His Ile Arg
20

<210> 394

<211> 230

<212> DNA

<213> Conus eburneus

<220>

<221> CDS

<222> (7)..(195)

<400> 394

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gat tcc ttc act tca gtt cgt act tcc gtt ggc agg agt gct gca gcc 96
Asp Ser Phe Thr Ser Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala
15 20 25 30

aac gcg ttt gac cgg atc gct ctg acc gcc agg caa gat tat tgc tgt 144
Asn Ala Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys

35 40 45
acc att ccc agc tgt tgg gat cgc tat aaa gag aga tgt aga cac ata 192
Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile
50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230
Arg

<210> 395
<211> 63
<212> PRT
<213> Conus eburneus

<400> 395
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Asp Ser
1 5 10 15

Phe Thr Ser Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala Asn Ala
20 25 30

Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys Thr Ile
35 40 45

Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile Arg
50 55 60

<210> 396
<211> 22
<212> PRT
<213> Conus eburneus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 16 is Glu or
gamma-carboxy-Glu; Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at
residue 11 is Trp (D or L) or bromo-Trp (D or L);

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residues 3 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 396
Xaa Asp Xaa Cys Cys Thr Ile Xaa Ser Cys Xaa Asp Arg Xaa Lys Xaa
1 5 10 15

Arg Cys Arg His Ile Arg
20

<210> 397
<211> 221
<212> DNA
<213> Conus miles

<220>
<221> CDS
<222> (7)..(177)

<400> 397
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act gct gtt 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val
1 5 10

ctt cca gtc act tta gat cgt gca tct gat gga agg aat gca gca gcc 96
Leu Pro Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala
15 20 25 30

aac gcc aaa acg cct cgc ctg atc gcg cca ttc atc agg gat tat tgc 144
Asn Ala Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys
35 40 45

tgt cat aga ggt ccc tgt atg gta tgg tgt ggt tgaagccgct gctgctccag 197
Cys His Arg Gly Pro Cys Met Val Trp Cys Gly
50 55

gaccctctga accacgacct cgag 221

<210> 398
<211> 57
<212> PRT
<213> Conus miles

<400> 398
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro
1 5 10 15

Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
20 25 30

Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His
35 40 45

Arg Gly Pro Cys Met Val Trp Cys Gly
50 55

<210> 399
<211> 13
<212> PRT
<213> Conus miles

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at residue 12 is Trp
(D or L) or bromo-Trp (D or L); Xaa at residue 2 is Tyr, 125I-Tyr
, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 399
Asp Xaa Cys Cys His Arg Gly Xaa Cys Met Val Xaa Cys
1 5 10

<210> 400
<211> 218
<212> DNA
<213> Conus jDedius

<220>

<221> CDS

<222> (7)..(174)

<400> 400

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val

1

5

10

gtt tcc aac tct tca gat cgt ggt cca gca tct aat aaa agg aag aat 96

Val Ser Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn

15

20

25

30

gcc gca atg ctt gac atg atc gct caa cac gcc ata agg ggt tgc tgt 144

Ala Ala Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys

35

40

45

tcc gat cct cgc tgt aga tat aga tgt cgt tgaagacgct gctgctccag 194

Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg

50

55

gaccctctga accacgacct cgag 218

<210> 401

<211> 56

<212> PRT

<213> Conus jDedius

<400> 401

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

1

5

10

15

Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn Ala Ala

20

25

30

Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys Ser Asp

35

40

45

Pro Arg Cys Arg Tyr Arg Cys Arg

50

55

<210> 402

<211> 13

<212> PRT

<213> Conus jDedius

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 6 is Pro or hydroxy-Pro;Xaa at residue 10 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 402

Gly Cys Cys Ser Asp Xaa Arg Cys Arg Xaa Arg Cys Arg

1

5

10

<210> 403

<211> 17

<212> PRT

<213> Conus omaria

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<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro

<400> 403
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
1          5          10          15

Gly

<210> 404
<211> 17
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro; C terminus contains free hydroxyl

<400> 404
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
1          5          10          15

Gly

<210> 405
<211> 224
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (7)..(189)

<400> 405
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc          48
      Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
      1          5          10

act tca gat cgt gta tct aat ggc agg aaa gct gca gcc aaa ttc aaa          96
Thr Ser Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys
15          20          25          30

gcg cct gcc ctg atg gag ctg tcc gtc agg caa gga tgc tgt tca gat          144
Ala Pro Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp
      35          40          45

cct gcc tgt gcc gtg agc aat cca gac atc tgt ggc gga gga cgc          189
Pro Ala Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg
      50          55          60

tgatgctcca ggaccctctg aaccacgacc tcgag          224

<210> 406
<211> 61
<212> PRT
<213> Conus quercinus

```

<400> 406

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Thr Ser
 1 5 10 15

Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys Ala Pro
 20 25 30

Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp Pro Ala
 35 40 45

Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg
 50 55 60

<210> 407

<211> 19

<212> PRT

<213> *Conus quercinus*

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 7 and 14 is Pro or hydroxy-Pro

<400> 407

Xaa Gly Cys Cys Ser Asp Xaa Ala Cys Ala Val Ser Asn Xaa Asp Ile
 1 5 10 15

Cys Gly Gly

<210> 408

<211> 230

<212> DNA

<213> *Conus bandanus*

<220>

<221> CDS

<222> (7)..(186)

<400> 408

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ttc act tca aat cgt gca ttt cgt cgt agg aat gcc gta gcc 96
 Val Ser Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala
 15 20 25 30

aaa gcg tct gac ctg atc gct ctg aac gcc agg aga cca gaa tgc tgt 144
 Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys
 35 40 45

act cat cct gcc tgt cac gtg agt cat cca gaa ctc tgt ggt 186
 Thr His Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly
 50 55 60

tgaagacgct gacgctccag gaccctctga accacgacct cgag 230

<210> 409

<211> 60
 <212> PRT
 <213> Conus bandanus

<400> 409
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala Lys Ala
 20 25 30
 Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys Thr His
 35 40 45
 Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly
 50 55 60

<210> 410
 <211> 17
 <212> PRT
 <213> Conus bandanus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro

<400> 410
 Xaa Xaa Cys Cys Thr His Xaa Ala Cys His Val Ser His Xaa Xaa Leu
 1 5 10 15

Cys

<210> 411
 <211> 242
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (7)..(198)

<400> 411
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc ttc act tca aat cgt gtt ctg gat cca gca ttt cgt cgt agg 96
 Val Ser Phe Thr Ser Asn Arg Val Leu Asp Pro Ala Phe Arg Arg Arg
 15 20 25 30
 aat gcc gca gcc aaa gcg tct gac ctg atc gct ctg aac gcc agg aga 144
 Asn Ala Ala Ala Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg
 35 40 45
 cca gaa tgc tgt act cat cct gcc tgt cac gtg agt aat cca gaa ctc 192
 Pro Glu Cys Cys Thr His Pro Ala Cys His Val Ser Asn Pro Glu Leu
 50 55 60

tgt ggc tgaagacgct gatgctccag gaccctctga accacgacct cgag 242
Cys Gly

<210> 412
<211> 64
<212> PRT
<213> Conus marmoreus

<400> 412
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Phe Thr Ser Asn Arg Val Leu Asp Pro Ala Phe Arg Arg Arg Asn Ala
20 25 30
Ala Ala Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu
35 40 45
Cys Cys Thr His Pro Ala Cys His Val Ser Asn Pro Glu Leu Cys Gly
50 55 60

<210> 413
<211> 17
<212> PRT
<213> Conus marmoreus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro

<400> 413
Xaa Xaa Cys Cys Thr His Xaa Ala Cys His Val Ser Asn Xaa Xaa Leu
1 5 10 15

Cys

<210> 414
<211> 218
<212> DNA
<213> Conus miles

<220>
<221> CDS
<222> (7)..(174)

<400> 414
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc gtc act tca tat cgt gca tct cat ggc agg aag gac gca gcc 96
Val Ser Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala
15 20 25 30

gac ctg agc gct ctg aac gac aac aat aat tgc tgt aac cat cct gcc 144
Asp Leu Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala
35 40 45

tgt gcc ggg aaa aat tca gat ctt tgt ggt tgaagacgct gctgctccag 194
 Cys Ala Gly Lys Asn Ser Asp Leu Cys Gly
 50 55

gaccctctga accacgacct cgag 218

<210> 415
 <211> 56
 <212> PRT
 <213> Conus miles

<400> 415
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala Asp Leu
 20 25 30

Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala Cys Ala
 35 40 45

Gly Lys Asn Ser Asp Leu Cys Gly
 50 55

<210> 416
 <211> 15
 <212> PRT
 <213> Conus miles

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 5 is Pro or hydroxy-Pro

<400> 416
 Cys Cys Asn His Xaa Ala Cys Ala Gly Lys Asn Ser Asp Leu Cys
 1 5 10 15

<210> 417
 <211> 16
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 11 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is
 Pro or hydroxy-Pro; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 417
 Gly Cys Cys Xaa His Xaa Thr Cys His Leu Xaa His Ser Asn Leu Cys
 1 5 10 15

<210> 418
 <211> 224
 <212> DNA
 <213> Conus nobilis

<220>

<221> CDS
 <222> (7)..(189)

<220>
 <221> misc_feature
 <222> (1)..(224)
 <223> n is unknown

<400> 418
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc ttc act tca gat cgt gca tct gat ggc agg aat gcc gca gcc 96
 Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala
 15 20 25 30
 aaa gct tct gac ctg att gct ttg acc gtc agg gga tgc tgt gag cga 144
 Lys Ala Ser Asp Leu Ile Ala Leu Thr Val Arg Gly Cys Cys Glu Arg
 35 40 45
 cct ccc tgt cgc tgg caa aat cca gat ctt tgt ggt gga agg cgc 189
 Pro Pro Cys Arg Trp Gln Asn Pro Asp Leu Cys Gly Gly Arg Arg
 50 55 60
 tganattcca ggaccctctg aaccacgacc tcgag 224

<210> 419
 <211> 61
 <212> PRT
 <213> Conus nobilis

<400> 419
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Lys Ala
 20 25 30
 Ser Asp Leu Ile Ala Leu Thr Val Arg Gly Cys Cys Glu Arg Pro Pro
 35 40 45
 Cys Arg Trp Gln Asn Pro Asp Leu Cys Gly Gly Arg Arg
 50 55 60

<210> 420
 <211> 17
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residues 6,
 7 and 13 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L)
 or bromo-Trp (D or L)

<400> 420
 Gly Cys Cys Xaa Arg Xaa Xaa Cys Arg Xaa Gln Asn Xaa Asp Leu Cys
 1 5 10 15

Gly

<210> 421
 <211> 233
 <212> DNA
 <213> Conus atlanticus

<220>
 <221> CDS
 <222> (7)..(198)

<400> 421
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc aca gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

 gtt tcc ttc act tca gat agt gca ttt gat agc agg aat gtc gca gcc 96
 Val Ser Phe Thr Ser Asp Ser Ala Phe Asp Ser Arg Asn Val Ala Ala
 15 20 25 30

 aac gac aaa gtg tct gac atg atc gct ctg acc gcc agg aga aca tgc 144
 Asn Asp Lys Val Ser Asp Met Ile Ala Leu Thr Ala Arg Arg Thr Cys
 35 40 45

 tgt tcc cgt cct acc tgt aga atg gaa tat cca gaa ctt tgt ggt gga 192
 Cys Ser Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys Gly Gly
 50 55 60

 aga cgc tgatactcca ggaccctctg aaccacgacc togag 233
 Arg Arg

<210> 422
 <211> 64
 <212> PRT
 <213> Conus atlanticus

<400> 422
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

 Phe Thr Ser Asp Ser Ala Phe Asp Ser Arg Asn Val Ala Ala Asn Asp
 20 25 30

 Lys Val Ser Asp Met Ile Ala Leu Thr Ala Arg Arg Thr Cys Cys Ser
 35 40 45

 Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys Gly Gly Arg Arg
 50 55 60

<210> 423
 <211> 17
 <212> PRT
 <213> Conus atlanticus

<220>
 <221> PEPTIDE
 <222> (1)..(17)

<223> Xaa at residues 11 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 6 and 13 is Pro or hydroxy-Pro; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 423

Thr Cys Cys Ser Arg Xaa Thr Cys Arg Met Xaa Xaa Xaa Xaa Leu Cys
1 5 10 15

Gly

<210> 424

<211> 227

<212> DNA

<213> Conus quercinus

<220>

<221> CDS

<222> (7)..(192)

<220>

<221> misc_feature

<222> (1)..(227)

<223> n is unknown

<400> 424

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca atc acg gtg 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val
1 5 10

ggt tcc ttc acc tca gat cat gca tct gat ggc agg aat acc gca gcc 96
Val Ser Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala
15 20 25 30

aac gac aaa gcg tct aaa ctg atg gct ctt acg aac gaa tgc tgt gac 144
Asn Asp Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp
35 40 45

aat cct ccg tgc aag tcg agt aat cca gat ttg tgt gac tgg aga agc 192
Asn Pro Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser
50 55 60

tgatgctcca ggaccctntg aaccacgacc tcgag 227

<210> 425

<211> 62

<212> PRT

<213> Conus quercinus

<400> 425

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala Asn Asp
20 25 30

Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp Asn Pro
35 40 45

Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser

50 55 60

<210> 426
 <211> 21
 <212> PRT
 <213> *Conus quercinus*

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp (D or L) or bromo-Trp (D or L)

<400> 426
 Asn Xaa Cys Cys Asp Asn Xaa Xaa Cys Lys Ser Ser Asn Xaa Asp Leu
 1 5 10 15
 Cys Asp Xaa Arg Ser
 20

<210> 427
 <211> 221
 <212> DNA
 <213> *Conus leopardus*

<220>
 <221> CDS
 <222> (7)..(177)

<400> 427
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acg gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc ctc act tta gat cgt gca tct ggt ggc agg aga tct gga gcc 96
 Val Ser Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala
 15 20 25 30
 gac aac atg att gct ctt ctg atc atc aga aaa tgc tgt tcc aat ccc 144
 Asp Asn Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro
 35 40 45
 gcc tgt aac agg tat aat cca gca att tgt gat tgaagacgct aatgctccag 197
 Ala Cys Asn Arg Tyr Asn Pro Ala Ile Cys Asp
 50 55
 gaccctctga accacgacct cgag 221

<210> 428
 <211> 57
 <212> PRT
 <213> *Conus leopardus*

<400> 428
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala Asp Asn
 20 25 30

Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro Ala Cys
 35 40 45

Asn Arg Tyr Asn Pro Ala Ile Cys Asp
 50 55

<210> 429
 <211> 16
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residues 5 and 12 is Pro or hydroxy-Pro; Xaa at residue 10
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
 phospho-Tyr

<400> 429
 Cys Cys Ser Asn Xaa Ala Cys Asn Arg Xaa Asn Xaa Ala Ile Cys Asp
 1 5 10 15

<210> 430
 <211> 224
 <212> DNA
 <213> Conus emaciatus

<220>
 <221> CDS
 <222> (7)..(180)

<400> 430
 ggatcc atg ttc acc gtg ttt ctg ttg gtt ctc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Leu Leu Ala Thr Thr Val
 1 5 10

act tta cat cgt gca tct aat ggc agg aat gcc gca gcc agc agg aaa 96
 Thr Leu His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys
 15 20 25 30
 gcg tct gcc ctg atc gct cag atc gcc ggt aga gac tgc tgt aac ttt 144
 Ala Ser Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe
 35 40 45

cct gct tgt gcc gcg agt aat cca ggc ctt tgt act tgaagacgct 190
 Pro Ala Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr
 50 55

gctgctccag gaccctctga accacgacct cgag 224

<210> 431
 <211> 58
 <212> PRT
 <213> Conus emaciatus

<400> 431
 Met Phe Thr Val Phe Leu Leu Val Leu Leu Ala Thr Thr Val Thr Leu
 1 5 10 15

His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys Ala Ser

20	25	30	
Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe Pro Ala			
35	40	45	
Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr			
50	55		
<210> 432			
<211> 17			
<212> PRT			
<213> Conus emaciatus			
<220>			
<221> PEPTIDE			
<222> (1)..(17)			
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro			
<400> 432			
Asp Cys Cys Asn Phe Xaa Ala Cys Ala Ala Ser Asn Xaa Gly Leu Cys			
1	5	10	15
Thr			
<210> 433			
<211> 215			
<212> DNA			
<213> Conus victor			
<220>			
<221> CDS			
<222> (7)..(180)			
<400> 433			
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc atc			48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile			
1	5	10	
ggt tcc tcc act tta gat cgt gca tct gat ggc atg aat gct gca gcg			
Val Ser Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala			96
15	20	25	30
tct gac ctg atc gct ctg agc atc agg aga tgc tgt tct tct cct ccc			144
Ser Asp Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro			
35	40	45	
tgt ttc gcg agt aat cca gct tgt ggt aga cga cgc tgatgctcca			
Cys Phe Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg			190
50	55		
ggaccctctg aaccacgacc tcgag			
			215
<210> 434			
<211> 58			
<212> PRT			
<213> Conus victor			
<400> 434			
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser			
1	5	10	15

Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala Ser Asp
 20 25 30

Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro Cys Phe
 35 40 45

Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg
 50 55

<210> 435
 <211> 14
 <212> PRT
 <213> Conus victor

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residues 5, 6 and 13 is Pro or hydroxy-Pro

<400> 435
 Cys Cys Ser Ser Xaa Xaa Cys Phe Ala Ser Asn Xaa Ala Cys
 1 5 10

<210> 436
 <211> 230
 <212> DNA
 <213> Conus cinereus gubba

<220>
 <221> CDS
 <222> (7)..(195)

<400> 436
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act atc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile
 1 5 10

gtt tcc tcc act tca ggt cat gca ttt gat ggc agg aat gct gca gcc 96
 Val Ser Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala
 15 20 25 30

gac tac aaa ggg tct gaa ttg ctt gct atg acc gtc agg gga gga tgc 144
 Asp Tyr Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys
 35 40 45

tgt tcc ttt cct ccc tgt atc gca aat aat cct ttt tgt gct gga aga 192
 Cys Ser Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg
 50 55 60

cgc tgatgctcca ggaccctctg aaccaagacc tcgag 230
 Arg

<210> 437
 <211> 63
 <212> PRT
 <213> Conus cinereus gubba

<400> 437
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser
 1 5 10 15

Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr
 20 25 30

Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys Cys Ser
 35 40 45

Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg Arg
 50 55 60

<210> 438

<211> 17

<212> PRT

<213> Conus cinereus gubba

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro

<400> 438

Gly Gly Cys Cys Ser Phe Xaa Xaa Cys Ile Ala Asn Asn Xaa Phe Cys
 1 5 10 15

Ala

<210> 439

<211> 221

<212> DNA

<213> Conus flavidus

<220>

<221> CDS

<222> (7)..(177)

<400> 439

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val
 1 5 10

act tta gat cgt gca tct cat ggc agg tat atc cca gtc gtc gac aga 96
 Thr Leu Asp Arg Ala Ser His Gly Arg Tyr Ile Pro Val Val Asp Arg
 15 20 25 30

gcg tct gcc ctg atg gct cag gcc gac ctt aga ggt tgc tgt tcc aat 144
 Ala Ser Ala Leu Met Ala Gln Ala Asp Leu Arg Gly Cys Cys Ser Asn
 35 40 45

cct cct tgt tcc tat ctt aat cca gcc tgt ggt taaagacgct gccgctccag 197
 Pro Pro Cys Ser Tyr Leu Asn Pro Ala Cys Gly
 50 55

gaccctctga accacgacct cgag 221

<210> 440

<211> 57

<212> PRT

<213> Conus flavidus

<400> 440

Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu

1	5					10					15				
Asp	Arg	Ala	Ser	His	Gly	Arg	Tyr	Ile	Pro	Val	Val	Asp	Arg	Ala	Ser
			20					25					30		
Ala	Leu	Met	Ala	Gln	Ala	Asp	Leu	Arg	Gly	Cys	Cys	Ser	Asn	Pro	Pro
		35					40					45			
Cys	Ser	Tyr	Leu	Asn	Pro	Ala	Cys	Gly							
	50					55									

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<210> 441
<211> 15
<212> PRT
<213> Conus flavidus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro; Xaa at residue
      10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr

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<400> 441
Gly Cys Cys Ser Asn Xaa Xaa Cys Ser Xaa Leu Asn Xaa Ala Cys
1 5 10 15

<210>	442
<211>	221
<212>	DNA
<213>	Conus emaciatus

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<220>
<221> CDS
<222> {7}..{177}
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<400> 442
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val
1 5 10

act	tta	gat	cgt	gca	tct	cat	ggc	agg	tat	gcc	gca	gtc	gtc	aac	aga	96
Thr	Leu	Asp	Arg	Ala	Ser	His	Gly	Arg	Tyr	Ala	Ala	Val	Val	Asn	Arg	
15					20					25					30	
gcg	tct	gcc	ctg	atg	gct	cat	gcc	gcc	ctt	cga	gat	tgc	tgt	tcc	gat	144
Ala	Ser	Ala	Leu	Met	Ala	His	Ala	Ala	Leu	Arg	Asp	Cys	Cys	Ser	Asp	
				35					40					45		

cct cct tgt gct cat aat aat cca gac tgt cgt taaagacgct gctgctccag 197
Pro Pro Cys Ala His Asn Asn Pro Asp Cys Arg
50 55

gaccctctga accacgacct cgag 221

<210>	443
<211>	57
<212>	PRT
<213>	Conus emaciatus

<400> 443

Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu
1 5 10 15

Asp Arg Ala Ser His Gly Arg Tyr Ala Ala Val Val Asn Arg Ala Ser
20 25 30

Ala Leu Met Ala His Ala Ala Leu Arg Asp Cys Cys Ser Asp Pro Pro
35 40 45

Cys Ala His Asn Asn Pro Asp Cys Arg
50 55

<210> 444
<211> 16
<212> PRT
<213> Conus emaciatius

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro

<400> 444
Asp Cys Cys Ser Asp Xaa Xaa Cys Ala His Asn Asn Xaa Asp Cys Arg
1 5 10 15

<210> 445
<211> 230
<212> DNA
<213> Conus generalis

<220>
<221> CDS
<222> (7)..(195)

<400> 445
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc ttc act tca gat cgt ggg tct gat ggc agg aat gcc gca gcc 96
Val Ser Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala
15 20 25 30

aag gac aaa gcg tct gac ctg gtc gct ctg acc gtc aag gga tgc tgt 144
Lys Asp Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys
35 40 45

tct aat cct ccc tgt tac gcg aat aat caa gcc tat tgt aat gga aga 192
Ser Asn Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg
50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230
Arg

<210> 446
<211> 63
<212> PRT
<213> Conus generalis

<400> 446

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp
 20 25 30

Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys Ser Asn
 35 40 45

Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg Arg
 50 55 60

<210> 447

<211> 17

<212> PRT

<213> *Conus generalis*

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 9
 and 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 447

Gly Cys Cys Ser Asn Xaa Xaa Cys Xaa Ala Asn Asn Gln Ala Xaa Cys
 1 5 10 15

Asn

<210> 448

<211> 212

<212> DNA

<213> *Conus wittigi*

<220>

<221> CDS

<222> (7)..(195)

<400> 448

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

ggt tcc ccc act aga gat cgt gca tct ggt gtc agg aat gtt gtt gca 96
 Val Ser Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala
 15 20 25 30

aca agc ttt cag act ctg acc cac gat gaa tgc tgt gca cac cct tcc 144
 Thr Ser Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser
 35 40 45

tgt tgg aag gcc gaa gac ctg att tgt act aat caa cgt cgc agg acc 192
 Cys Trp Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr
 50 55 60

ctc tgaaccacga cctcgag 212
 Leu

<210> 449
 <211> 63
 <212> PRT
 <213> Conus wittigi

<400> 449
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala Thr Ser
 20 25 30
 Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser Cys Trp
 35 40 45
 Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr Leu
 50 55 60

<210> 450
 <211> 25
 <212> PRT
 <213> Conus wittigi

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residues 2 and 13 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or bromo-Trp (D or L)

<400> 450
 Asp Xaa Cys Cys Ala His Xaa Ser Cys Xaa Lys Ala Xaa Asp Leu Ile
 1 5 10 15
 Cys Thr Asn Gln Arg Arg Arg Thr Leu
 20 25

<210> 451
 <211> 230
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (7)..(195)

<400> 451
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ttc act tca gat cgt gcg tct gaa ggc agg aat gct gca gcc 96
 Val Ser Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Ala
 15 20 25 30

aag gac aaa gcg tct gac ctg gtg gct ctg aga gtc agg gga tgc tgt 144
 Lys Asp Lys Ala Ser Asp Leu Val Ala Leu Arg Val Arg Gly Cys Cys
 35 40 45

gcc att cgt gaa tgt cgc ttg cag aat gca gcg tat tgt ggt gga ata 192
 Ala Ile Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile
 50 55 60

tcc tgatgctcca ggaccctctg aaccacgacc tcgag 230
 Ser

<210> 452
 <211> 63
 <212> PRT
 <213> Conus characteristicus

<400> 452
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Ala Lys Asp
 20 25 30

Lys Ala Ser Asp Leu Val Ala Leu Arg Val Arg Gly Cys Cys Ala Ile
 35 40 45

Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile Ser
 50 55 60

<210> 453
 <211> 20
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(20)
 <223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residue 15 is
 s Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-ph
 osphe-Tyr

<400> 453
 Gly Cys Cys Ala Ile Arg Xaa Cys Arg Leu Gln Asn Ala Ala Xaa Cys
 1 5 10 15

Gly Gly Ile Ser
 20

<210> 454
 <211> 568
 <212> DNA
 <213> Conus betulinus

<220>
 <221> CDS

<222> (395) .. (508)

 $\langle 220 \rangle$

<221> misc feature

$$\langle 222 \rangle \quad (1) \cdot \cdot (568)$$

<223> n is unknown

<400> 454

agtaattnat atannagaaa gnaananaaa annatanaga atttaagtaa tntaagaann 60

qaganagtqa atagnagnta agtagannaa ganaggtaga naqnangn qganntagn 120

taataqatan nntatngaga nattantagc ngtatanana agaaaagagg gnaanngaaa 180

tgngngaann ataantanta nngatngann ngnaagtgnn aagngtanaa ggaanaacaa 240

antngttqtn taatntqnnnt gngtqtgtnt qtqtgngtgt qtqtgtgtgn qtgngtgtgt 300

ntgtgngnnt gtgtgngngn gngngtgtgt gtgtgngtgt gtgtgttgtgt gtgtgttgtgt 360

gtgtgtgtgt gngtgtgtgg ttctggatcc agca tct ggt ggc agg aag gct gca 415
Ser Gly Gly Arg Lys Ala Ala
1 5

gcc aaa gcg tct aac cgg atc gct ctg acc gtc agg agt gca aca tgc 463
Ala Lys Ala Ser Asn Arg Ile Ala Leu Thr Val Arg Ser Ala Thr Cys
10 15 20

tgt tat tat cct ccc tgt tac gag gct tat cca gaa agt tgt ctg 508
 Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala Tyr Pro Glu Ser Cys Leu
 25 30 35

taacgtqaat catccagacc tttgtggctg aagaccctga tgctccaggg gcaagttcaa 568

<210> 455

<211> 38

<212> PRT

<213> Conus betulinus

<400> 455

Ser Gly Gly Arg Lys Ala Ala Ala Lys Ala Ser Asn Arg Ile Ala Leu
1 5 10 15

Thr Val Arg Ser Ala Thr Cys Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala
20 25 30

Tyr Pro Glu Ser Cys Leu
35

<210> 456

<211> 19

<212> PRT

<213> *Conus betulinus*

<220>

<221> PEPTIDE

<222> (1) . . (19)

<223> Xaa at residues 12 and 16 is Glu or gamma-carboxy-Glu; Xaa at residues 8, 9 and 13 is Pro or hydroxy-Pro; Xaa at residues 6, 7, 11 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty

r or O-phospho-Tyr

<400> 456

Ser Ala Thr Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Xaa Xaa
1 5 10 15

Ser Cys Leu

<210> 457

<211> 29

<212> PRT

<213> Conus textile

<400> 457

Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys
1 5 10 15

Asp Trp Trp Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe
20 25

<210> 458

<211> 31

<212> PRT

<213> Conus ammiralis

<400> 458

Gly Met Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro
1 5 10 15

Ser Glu Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
20 25 30

<210> 459

<211> 36

<212> PRT

<213> Conus ammiralis

<400> 459

Trp Arg Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp
1 5 10 15

Gln Gln Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu
20 25 30

Trp Asp Asp Arg
35

<210> 460

<211> 25

<212> PRT

<213> Conus ammiralis

<400> 460

Asn Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys
1 5 10 15

Ser Trp Asp Cys Asp Val Val Cys Ser
20 25

<210> 461

<211> 39
 <212> PRT
 <213> Conus ammiralis

<400> 461
 Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys
 1 5 10 15
 Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu
 20 25 30
 Met Arg Phe Pro Pro Asp Trp
 35

<210> 462
 <211> 29
 <212> PRT
 <213> Conus ammiralis

<400> 462
 Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys
 1 5 10 15
 Asp Trp Trp Thr Cys Ser Ala Arg Thr Gly Arg Cys Phe
 20 25

<210> 463
 <211> 26
 <212> PRT
 <213> Conus ammiralis

<400> 463
 Leu Cys Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys
 1 5 10 15
 Ser Trp Asn Cys His Asn Gly His Cys Thr
 20 25

<210> 464
 <211> 27
 <212> PRT
 <213> Conus ammiralis

<400> 464
 Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys Ser
 1 5 10 15
 Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
 20 25

<210> 465
 <211> 32
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 14 and 26 is gamma-carboxy-Glu; Xaa at residue 31
 is hydroxy-Pro

<400> 465

Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15

Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 466

<211> 32

<212> PRT

<213> *Conus gloriamaris*

<400> 466

Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser Pro Gly Ala Gln Cys Cys
 1 5 10 15

Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu
 20 25 30

<210> 467

<211> 27

<212> PRT

<213> *Conus textile*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa is gamma-carboxy-Glu

<400> 467

Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr
 1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 468

<211> 29

<212> PRT

<213> *Conus marmoreus*

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa is gamma-carboxy-Glu

<400> 468

Asn Gly Gln Cys Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Xaa
 1 5 10 15

Cys Cys Ser Leu Asp Cys Glu Met Tyr Cys Thr Gln Ile
 20 25

<210> 469

<211> 27

<212> PRT

<213> *Conus marmoreus*

<220>

<221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa is gamma-carboxy-Glu

<400> 469
 Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Xaa Cys Cys Ser
 1 5 10 15
 Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 470
 <211> 26
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa is gamma-carboxy-Glu

<400> 470
 Asn Gly Gly Cys Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Xaa
 1 5 10 15
 Cys Cys Ser Met Ser Cys Asp Met Tyr Cys
 20 25

<210> 471
 <211> 33
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 1, 10 and 33 is bromo-Trp; Xaa at residues 5, 6,
 15 and 26 is gamma-carboxy-Glu

<400> 471
 Xaa Phe Gly His Xaa Xaa Cys Thr Tyr Xaa Leu Gly Pro Cys Xaa Val
 1 5 10 15
 Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu
 20 25 30

Xaa

<210> 472
 <211> 31
 <212> PRT
 <213> Conus radiatus

<400> 472
 Trp Trp Gly Gly Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro
 1 5 10 15
 Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
 20 25 30

<210> 473
 <211> 26
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residues 3 and 8 is hydroxy-Pro; Xaa at residues 7 and 14
 is gamma-carboxy-Glu

<400> 473
 Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
 1 5 10 15
 Ser Trp Asn Cys Tyr Asn Gly His Cys Thr
 20 25

<210> 474
 <211> 28
 <212> PRT
 <213> Conus textile

<400> 474
 Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser Gln Cys Cys
 1 5 10 15
 Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg
 20 25

<210> 475
 <211> 34
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa is gamma-carboxy-Glu

<400> 475
 Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser Xaa
 1 5 10 15
 Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro Pro
 20 25 30

Asp Trp

<210> 476
 <211> 31
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa is gamma-carboxy-Glu

<400> 476

Gly Met Trp Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro
 1 5 10 15

Ser Xaa Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
 20 25 30

<210> 477
 <211> 34
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa is gamma-carboxy-Glu

<400> 477
 Asp Trp Trp Asp Asp Gly Cys Ser Val Trp Gly Pro Cys Thr Val Asn
 1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Glu Thr Cys Ile Phe Gly Trp
 20 25 30

Glu Val

<210> 478
 <211> 39
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(39)
 <223> Xaa is gamma-carboxy-Glu

<400> 478
 Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu Cys Ser Arg
 1 5 10 15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Glu Leu
 20 25 30

Met Pro Phe Pro Pro Asp Trp
 35

<210> 479
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa is gamma-carboxy-Glu

<400> 479
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser
 1 5 10 15

Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe

20

25

<210> 480
 <211> 43
 <212> PRT
 <213> Conus characteristicus

<400> 480
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Ser Cys Gln
 35 40

<210> 481
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<400> 481
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 482
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<400> 482
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 483
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<400> 483
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys

35 40

<210> 484
<211> 42
<212> PRT
<213> Conus characteristicus

<400> 484
Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly
1 5 10 15
Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
20 25 30
His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
35 40

<210> 485
<211> 42
<212> PRT
<213> Conus characteristicus

<400> 485
Gly Cys Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly
1 5 10 15
Thr Cys Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu
20 25 30
Gly Thr Tyr Ser Gly Cys Val Cys Ile Cys
35 40

<210> 486
<211> 45
<212> PRT
<213> Conus lacterculatus

<400> 486
Gln Ser Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly
1 5 10 15
Lys Cys Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg
20 25 30
Gly Ser Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
35 40 45

<210> 487
<211> 48
<212> PRT
<213> Conus monachus

<400> 487
Gln Cys Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys
1 5 10 15
Asn Gly Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg
20 25 30
Val Ser Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
35 40 45

35 40 45

<210> 488
<211> 41
<212> PRT
<213> *Conus purpurascens*

<400> 488
Gly Cys Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu
1 5 10 15
Cys Ile Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser
20 25 30
Arg Gly Cys Lys Cys Thr Cys Arg Glu
35 40

<210> 489
<211> 47
<212> PRT
<213> *Conus radiatus*

<400> 489
Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly
1 5 10 15
Glu Ser Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn
20 25 30
Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
35 40 45

<210> 490
<211> 44
<212> PRT
<213> *Conus radiatus*

<400> 490
Tyr Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val
1 5 10 15
Arg Asp Tyr Cys Asp Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys
20 25 30
Gly Phe Arg Gln Pro Gly Cys Gly Cys Ser Cys Leu
35 40

<210> 491
<211> 46
<212> PRT
<213> *Conus striolatus*

<400> 491
Gln Cys Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Cys Ala Asn Gly
1 5 10 15
Asp Cys Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser
20 25 30
Pro Gly Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
35 40 45

<210> 492
 <211> 44
 <212> PRT
 <213> Conus tulipa

<400> 492
 Phe Gly Pro Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser
 1 5 10 15
 Cys Glu Cys Met Ser Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile
 20 25 30
 Arg Glu Arg Gly Cys Ser Cys Thr Cys Pro Gly Thr
 35 40

<210> 493
 <211> 46
 <212> PRT
 <213> Conus tulipa

<400> 493
 Gly Cys Thr Gly Asn Cys Asp Trp Thr Cys Ser Gly Asp Cys Ser Cys
 1 5 10 15
 Gln Gly Thr Ser Asp Ser Cys His Cys Ile Pro Pro Lys Ser Ile Gly
 20 25 30
 Asn Arg Cys Arg Cys Gln Cys Lys Arg Lys Ile Glu Ile Asp
 35 40 45

<210> 494
 <211> 15
 <212> PRT
 <213> Conus textile

<400> 494
 Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu Thr
 1 5 10 15

<210> 495
 <211> 15
 <212> PRT
 <213> Conus textile

<400> 495
 Gly Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu Thr
 1 5 10 15

<210> 496
 <211> 20
 <212> PRT
 <213> Conus marmoreus

<400> 496
 Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile Lys
 1 5 10 15
 Glu Asn Asp Phe
 20

<210> 497
 <211> 11
 <212> PRT
 <213> Conus marmoreus

<400> 497
 Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
 1 5 10

<210> 498
 <211> 10
 <212> PRT
 <213> Conus marmoreus

<400> 498
 Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
 1 5 10

<210> 499
 <211> 10
 <212> PRT
 <213> Conus quercinus

<400> 499
 Gly Cys Cys Ala Arg Leu Thr Cys Cys Val
 1 5 10

<210> 500
 <211> 10
 <212> PRT
 <213> Conus quercinus

<400> 500
 Gly Cys Cys Ala Met Leu Thr Cys Cys Val
 1 5 10

<210> 501
 <211> 12
 <212> PRT
 <213> Conus purpurascens

<400> 501
 Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu
 1 5 10

<210> 502
 <211> 11
 <212> PRT
 <213> Conus characteristicus

<400> 502
 Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile
 1 5 10

<210> 503
 <211> 10
 <212> PRT
 <213> Conus characteristicus

<400> 503

Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile
1 5 10

<210> 504

<211> 13

<212> PRT

<213> Conus geographus

<400> 504

Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
1 5 10

<210> 505

<211> 13

<212> PRT

<213> Conus geographus

<400> 505

Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
1 5 10

<210> 506

<211> 15

<212> PRT

<213> Conus imperialis

<400> 506

Asp Trp Asn Ser Cys Cys Gly Lys Asn Pro Gly Cys Cys Pro Trp
1 5 10 15

<210> 507

<211> 11

<212> PRT

<213> Conus betulinus

<400> 507

Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His
1 5 10

<210> 508

<211> 12

<212> PRT

<213> Conus ammiralis

<400> 508

Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp
1 5 10

<210> 509

<211> 9

<212> PRT

<213> Conus dalli

<400> 509

Cys Cys Glu Tyr Trp Lys Leu Cys Cys
1 5

<210> 510

<211> 11

<212> PRT
 <213> Conus omaria

 <400> 510
 Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg
 1 5 10

 <210> 511
 <211> 11
 <212> PRT
 <213> Conus aulicus

 <400> 511
 Phe Cys Cys Pro Val Ile Arg Tyr Cys Cys Trp
 1 5 10

 <210> 512
 <211> 11
 <212> PRT
 <213> Conus aulicus

 <400> 512
 Phe Cys Cys Pro Phe Ile Arg Tyr Cys Cys Trp
 1 5 10

 <210> 513
 <211> 10
 <212> PRT
 <213> Conus aulicus

 <400> 513
 Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
 1 5 10

 <210> 514
 <211> 10
 <212> PRT
 <213> Conus aulicus

 <400> 514
 Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
 1 5 10

 <210> 515
 <211> 10
 <212> PRT
 <213> Conus nobilis

 <400> 515
 Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys
 1 5 10

 <210> 516
 <211> 9
 <212> PRT
 <213> Conus ammiralis

 <400> 516
 Cys Cys Pro Pro Val Ile Trp Cys Cys
 1 5

<210> 517
 <211> 11
 <212> PRT
 <213> Conus textile

<400> 517
 Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln
 1 5 10

<210> 518
 <211> 13
 <212> PRT
 <213> Conus aulicus

<400> 518
 Trp Asn Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys
 1 5 10

<210> 519
 <211> 13
 <212> PRT
 <213> Conus gloriamaris

<400> 519
 Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp Trp
 1 5 10

<210> 520
 <211> 11
 <212> PRT
 <213> Conus gloriamaris

<400> 520
 Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser
 1 5 10

<210> 521
 <211> 13
 <212> PRT
 <213> Conus dalli

<400> 521
 Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser
 1 5 10

<210> 522
 <211> 17
 <212> PRT
 <213> Conus spurius

<400> 522
 Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro
 1 5 10 15

Ser

<210> 523
 <211> 12
 <212> PRT

<213> Conus textile

<400> 523

Glx Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
1 5 10

<210> 524

<211> 11

<212> PRT

<213> Conus bandanus

<400> 524

Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
1 5 10

<210> 525

<211> 13

<212> PRT

<213> Conus pennaceus

<400> 525

Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
1 5 10

<210> 526

<211> 13

<212> PRT

<213> Conus pennaceus

<400> 526

Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser
1 5 10

<210> 527

<211> 12

<212> PRT

<213> Conus pennaceus

<400> 527

Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys
1 5 10

<210> 528

<211> 12

<212> PRT

<213> Conus episcopatus

<400> 528

Ser Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
1 5 10

<210> 529

<211> 13

<212> PRT

<213> Conus marmoreus

<400> 529

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu Pro Cys
1 5 10

<210> 530
 <211> 12
 <212> PRT
 <213> Conus pennaceus

<400> 530
 Leu Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn
 1 5 10

<210> 531
 <211> 13
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa is hydroxy-Pro

<400> 531
 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys
 1 5 10

<210> 532
 <211> 12
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa is hydroxy-Pro

<400> 532
 Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys
 1 5 10

<210> 533
 <211> 11
 <212> PRT
 <213> Conus bandanus

<400> 533
 Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 1 5 10

<210> 534
 <211> 12
 <212> PRT
 <213> Conus aulicus

<400> 534
 Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe Pro Cys
 1 5 10

<210> 535
 <211> 13
 <212> PRT
 <213> Conus textile

<400> 535
 Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
 1 5 10

<210> 536
 <211> 12
 <212> PRT
 <213> Conus textile

<400> 536
 Glx Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
 1 5 10

<210> 537
 <211> 12
 <212> PRT
 <213> Conus ammiralis

<400> 537
 Glx Ala Cys Cys Gly Phe Lys Met Cys Val Pro Cys
 1 5 10

<210> 538
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<400> 538
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 1 5 10

<210> 539
 <211> 14
 <212> PRT
 <213> Conus pennaceus

<400> 539
 Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn
 1 5 10

<210> 540
 <211> 12
 <212> PRT
 <213> Conus omaria

<400> 540
 Asp Val Cys Cys Tyr Val Arg Met Cys Pro Cys Arg
 1 5 10

<210> 541
 <211> 7
 <212> PRT
 <213> Conus imperialis

<400> 541
 Glx Cys Gly Gln Ala Trp Cys
 1 5

<210> 542
 <211> 8

<212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(8)
 <223> Xaa is hydroxy-Pro

<400> 542

Gly Cys Xaa Trp Gln Pro Val Cys
 1 5

<210> 543
 <211> 11
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa is hydroxy-Pro

<400> 543
 Glx Tyr Gly Cys Xaa Xaa Gly Leu Trp Cys His
 1 5 10

<210> 544
 <211> 10
 <212> PRT
 <213> Conus arenatus

<400> 544
 Ala Ser Gly Cys Pro Trp Arg Pro Trp Cys
 1 5 10

<210> 545
 <211> 11
 <212> PRT
 <213> Conus arenatus

<400> 545
 Glx Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp
 1 5 10

<210> 546
 <211> 9
 <212> PRT
 <213> Conus arenatus

<400> 546
 Ser Gly Cys Pro Trp Gln Pro Trp Cys
 1 5

<210> 547
 <211> 9
 <212> PRT
 <213> Conus arenatus

<400> 547

Ser Gly Cys Pro Trp His Pro Trp Cys
1 5

<210> 548
<211> 30
<212> PRT
<213> Conus ermineus

<220>
<221> PEPTIDE
<222> (1)..(30)
<223> Xaa is hydroxy-Pro

<400> 548
Gly Cys Cys Gly Lys Tyr Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys
1 5 10 15

Thr Val Gly Arg Xaa Xaa Tyr Cys Asp Arg Xaa Ser Gly Gly
20 25 30

<210> 549
<211> 25
<212> PRT
<213> Conus purpurascens

<400> 549
Gly Cys Cys Gly Ser Tyr Pro Asn Ala Ala Cys His Pro Cys Gly Cys
1 5 10 15

Lys Asp Arg Pro Ser Tyr Cys Gly Gln
20 25

<210> 550
<211> 23
<212> PRT
<213> Conus purpurascens

<400> 550
Glu Gly Cys Cys Ser Asn Pro Ala Cys His Pro Cys Gly Cys Lys Asp
1 5 10 15

Arg Pro Ser Tyr Cys Gly Gln
20

<210> 551
<211> 32
<212> PRT
<213> Conus arenatus

<400> 551
Val Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu Glu Glu Lys His
1 5 10 15

Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp
20 25 30

<210> 552
<211> 32
<212> PRT
<213> Conus arenatus

<400> 552

Ile	Val	Thr	Glu	Ala	Cys	Glu	Glu	Ser	Cys	Glu	Asp	Glu	Glu	Lys	His
1				5					10					15	

Cys	Cys	His	Val	Asn	Asn	Gly	Val	Pro	Ser	Cys	Ala	Val	Ile	Cys	Trp
			20					25					30		

<210> 553

<211> 32

<212> PRT

<213> Conus arenatus

<400> 553

Ile	Val	Thr	Glu	Ala	Cys	Glu	Glu	His	Cys	Glu	Asp	Glu	Glu	Gln	Phe
1				5					10					15	

Cys	Cys	Gly	Leu	Glu	Asn	Gly	Gln	Pro	Phe	Cys	Ala	Pro	Val	Cys	Phe
			20					25					30		

<210> 554

<211> 32

<212> PRT

<213> Conus arenatus

<400> 554

Val	Val	Thr	Gly	Ala	Cys	Glu	Glu	His	Cys	Glu	Asp	Glu	Glu	Lys	His
1				5					10					15	

Cys	Cys	Gly	Leu	Glu	Asn	Gly	Gln	Pro	Phe	Cys	Ala	Arg	Leu	Cys	Leu
			20					25					30		

<210> 555

<211> 32

<212> PRT

<213> Conus distans

<400> 555

Asn	Val	Asp	Gln	Glu	Cys	Ile	Asp	Ala	Cys	Gln	Leu	Glu	Asp	Lys	Asn
1				5					10					15	

Cys	Cys	Gly	Arg	Thr	Asp	Gly	Glu	Pro	Arg	Cys	Ala	Lys	Ile	Cys	Leu
			20					25					30		

<210> 556

<211> 32

<212> PRT

<213> Conus distans

<400> 556

Glu	Thr	Asp	Gln	Glu	Cys	Ile	Asp	Ile	Cys	Lys	Gln	Glu	Asp	Lys	Lys
1				5					10					15	

Cys	Cys	Gly	Arg	Ser	Asn	Gly	Glu	Pro	Thr	Cys	Ala	Lys	Ile	Cys	Leu
			20					25					30		

<210> 557

<211> 32

<212> PRT

<213> Conus distans

<400> 557

Glu	Thr	Asp	Gln	Glu	Cys	Ile	Asp	Thr	Cys	Glu	Gln	Glu	Asp	Lys	Lys
1				5					10					15	

Cys	Cys	Gly	Arg	Thr	Asn	Gly	Glu	Pro	Val	Cys	Ala	Lys	Ile	Cys	Phe
			20					25					30		

<210> 558

<211> 37

<212> PRT

<213> *Conus purpurascens*

<400> 558

Pro	Lys	Thr	Glu	Ala	Cys	Glu	Glu	Val	Cys	Glu	Leu	Glu	Glu	Lys	His
1				5					10					15	

Cys	Cys	Cys	Ile	Arg	Ser	Asp	Gly	Pro	Lys	Cys	Ser	Arg	Lys	Cys	Leu
			20					25					30		

Leu	Ser	Ile	Phe	Cys
				35

<210> 559

<211> 32

<212> PRT

<213> *Conus purpurascens*

<400> 559

Val	Val	Ser	Glu	Glu	Cys	Lys	Lys	Tyr	Cys	Lys	Lys	Gln	Asn	Lys	Asn
1				5					10					15	

Cys	Cys	Ser	Ser	Lys	His	Glu	Glu	Pro	Arg	Cys	Ala	Lys	Ile	Cys	Phe
			20					25					30		

<210> 560

<211> 32

<212> PRT

<213> *Conus sponsalis*

<400> 560

Ala	Val	Thr	Glu	Ala	Cys	Thr	Glu	Asp	Cys	Lys	Thr	Gln	Asp	Lys	Lys
1				5					10					15	

Cys	Cys	Gly	Glu	Met	Asn	Gly	Gln	His	Thr	Cys	Ala	Lys	Ile	Cys	Leu
			20					25					30		

<210> 561

<211> 37

<212> PRT

<213> *Conus tulipa*

<400> 561

Pro	Lys	Thr	Lys	Glu	Cys	Glu	Arg	Tyr	Cys	Glu	Leu	Glu	Glu	Lys	His
1				5					10					15	

Cys	Cys	Cys	Ile	Arg	Ser	Asn	Gly	Pro	Lys	Cys	Ser	Arg	Ile	Cys	Ile
			20					25					30		

Phe	Lys	Phe	Trp	Cys
-----	-----	-----	-----	-----

35

<210> 562
 <211> 36
 <212> PRT
 <213> Conus tulipa

<400> 562
 Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln Glu Glu Lys His
 1 5 10 15
 Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Pro Lys Cys Leu
 20 25 30

Gly Ile Asn Trp
 35

<210> 563
 <211> 9
 <212> PRT
 <213> Conus geographus

<400> 563
 Cys Phe Ile Arg Asn Cys Pro Lys Gly
 1 5

<210> 564
 <211> 9
 <212> PRT
 <213> Conus striatus

<400> 564
 Cys Ile Ile Arg Asn Cys Pro Arg Gly
 1 5

<210> 565
 <211> 28
 <212> PRT
 <213> Conus arenatus

<400> 565
 Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys
 1 5 10 15

Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser
 20 25

<210> 566
 <211> 27
 <212> PRT
 <213> Conus geographus

<400> 566
 Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly
 1 5 10 15

Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys
 20 25

<210> 567
 <211> 31

<212> PRT

<213> Conus characteristicus

<400> 567

Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser
1 5 10 15

Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr
20 25 30

<210> 568

<211> 23

<212> PRT

<213> Conus textile

<400> 568

Asn Cys Pro Tyr Cys Val Val Tyr Cys Cys Pro Pro Ala Tyr Cys Glu
1 5 10 15

Ala Ser Gly Cys Arg Pro Pro
20

<210> 569

<211> 27

<212> PRT

<213> Conus delesstii

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is hydroxy-Pro; Xaa at residues 13 and 16 is gamma-carboxy-Glu

<400> 569

Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa
1 5 10 15

Cys Cys Ser Gly Phe Cys Leu Ile Tyr Arg Cys
20 25

<210> 570

<211> 30

<212> PRT

<213> Conus lividus

<400> 570

Ser Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys Pro
1 5 10 15

Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val
20 25 30

<210> 571

<211> 35

<212> PRT

<213> Conus lividus

<400> 571

Asp Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys
1 5 10 15

Pro Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro
 20 25 30

Ser Gly Ile
 35

<210> 572

<211> 31

<212> PRT

<213> Conus miliaris

<400> 572

Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser
 1 5 10 15

Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser
 20 25 30

<210> 573

<211> 36

<212> PRT

<213> Conus miles

<400> 573

Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys
 1 5 10 15

Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val
 20 25 30

Pro Glu Asn Ser
 35

<210> 574

<211> 36

<212> PRT

<213> Conus miles

<400> 574

Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys
 1 5 10 15

Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val
 20 25 30

Pro Glu Asn Ser
 35

<210> 575

<211> 30

<212> PRT

<213> Conus pulicarius

<400> 575

Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His Asn Cys Cys
 1 5 10 15

Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys Thr
 20 25 30

<210> 576
 <211> 30
 <212> PRT
 <213> *Conus quercinus*

<400> 576
 Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys
 1 5 10 15
 Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
 20 25 30

<210> 577
 <211> 28
 <212> PRT
 <213> *Conus striatus*

<400> 577
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15
 Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
 20 25

<210> 578
 <211> 31
 <212> PRT
 <213> *Conus tessulatus*

<400> 578
 Ser Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys Pro
 1 5 10 15
 Asp Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu
 20 25 30

<210> 579
 <211> 27
 <212> PRT
 <213> *Conus textile*

<400> 579
 Lys Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys
 1 5 10 15
 Ala Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu
 20 25

<210> 580
 <211> 29
 <212> PRT
 <213> *Conus textile*

<400> 580
 Cys Val Glu Gln Trp Glu Val Cys Gly Ile Ile Leu Phe Ser Ser Ser
 1 5 10 15
 Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu
 20 25

<210> 581
 <211> 32
 <212> PRT
 <213> *Conus virgo*

<400> 581
 Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro
 1 5 10 15
 Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu
 20 25 30

<210> 582
 <211> 33
 <212> PRT
 <213> *Conus wittigi*

<400> 582
 Phe Gly Ser Phe Ile Pro Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile
 1 5 10 15
 Cys Cys Arg Pro Leu Arg Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln
 20 25 30

Val

<210> 583
 <211> 30
 <212> PRT
 <213> *Conus regius*

<400> 583
 Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys
 1 5 10 15
 Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln
 20 25 30

<210> 584
 <211> 34
 <212> PRT
 <213> *Conus radiatus*

<400> 584
 Ala Cys Lys Ser Asn Tyr Asp Cys Pro Gln Arg Phe Lys Cys Cys Ser
 1 5 10 15
 Tyr Thr Trp Asn Gly Ser Ser Gly Tyr Cys Lys Arg Val Cys Tyr Leu
 20 25 30

Tyr Arg

<210> 585
 <211> 24
 <212> PRT
 <213> *Conus purpurascens*

<220>
 <221> PEPTIDE

<222> (1)..(24)

<223> Xaa is hydroxy-Pro

<400> 585

Gly Xaa Xaa Cys Cys Leu Tyr Gly Ser Cys Arg Xaa Phe Xaa Gly Cys
1 5 10 15

Tyr Asn Ala Leu Cys Cys Arg Lys
20

<210> 586

<211> 24

<212> PRT

<213> Conus purpurascens

<400> 586

His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys
1 5 10 15

Ser Ser Ala Ser Cys Cys Gln Gly
20

<210> 587

<211> 36

<212> PRT

<213> Conus consors

<400> 587

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
1 5 10 15

Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro
20 25 30

Lys Arg Lys Pro
35

<210> 588

<211> 39

<212> PRT

<213> Conus aurisiacus

<400> 588

Glx Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr Asp
1 5 10 15

Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys Pro
20 25 30

Lys Lys Pro Lys Pro Gly Lys
35

<210> 589

<211> 37

<212> PRT

<213> Conus consors

<400> 589

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
1 5 10 15

Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro His
 20 25 30

Gln Arg Lys Lys Pro
 35

<210> 590

<211> 36

<212> PRT

<213> Conus magus

<400> 590

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
 1 5 10 15

Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro
 20 25 30

Lys Gly Lys Pro
 35

<210> 591

<211> 38

<212> PRT

<213> Conus aurisiacus

<400> 591

Glx Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr Asn
 1 5 10 15

Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro Pro
 20 25 30

Leu Lys Lys Lys Arg Pro
 35

<210> 592

<211> 29

<212> PRT

<213> Conus aurisiacus

<400> 592

Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr
 1 5 10 15

Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys
 20 25

<210> 593

<211> 13

<212> PRT

<213> Conus geographus

<400> 593

Glu Cys Cys His Pro Ala Cys Gly Lys His Tyr Ser Cys
 1 5 10

<210> 594

<211> 13

<212> PRT
 <213> Conus geographus

<400> 594
 Glu Cys Cys Asn Pro Ala Cys Gly Arg His Phe Ser Cys
 1 5 10

<210> 595
 <211> 22
 <212> PRT
 <213> Conus striatus

<400> 595
 Ala Tyr Cys Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr
 1 5 10 15

Ser Cys Ser Arg Thr Leu
 20

<210> 596
 <211> 14
 <212> PRT
 <213> Conus striatus

<400> 596
 Ala Tyr Cys Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys
 1 5 10

<210> 597
 <211> 22
 <212> PRT
 <213> Conus rattus

<400> 597
 Gly Cys Cys Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr
 1 5 10 15

Ser Cys Ser Arg Thr Leu
 20

<210> 598
 <211> 22
 <212> PRT
 <213> Conus arenatus

<400> 598
 Glx Asp Tyr Cys Cys Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu
 1 5 10 15

Arg Cys Arg His Ile Arg
 20

<210> 599
 <211> 22
 <212> PRT
 <213> Conus eburneus

<400> 599
 Glx Asp Tyr Cys Cys Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu
 1 5 10 15

Arg Cys Arg His Ile Arg
20

<210> 600
<211> 13
<212> PRT
<213> Conus miles

<400> 600
Asp Tyr Cys Cys His Arg Gly Pro Cys Met Val Trp Cys
1 5 10

<210> 601
<211> 13
<212> PRT
<213> Conus jDedius

<400> 601
Gly Cys Cys Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
1 5 10

<210> 602
<211> 17
<212> PRT
<213> Conus omaria

<400> 602
Gly Cys Cys Ser His Pro Ala Cys Asn Val Asn Asn Pro His Ile Cys
1 5 10 15

Gly

<210> 603
<211> 17
<212> PRT
<213> Conus omaria

<400> 603
Gly Cys Cys Ser His Pro Ala Cys Asn Val Asn Asn Pro His Ile Cys
1 5 10 15

Gly

<210> 604
<211> 19
<212> PRT
<213> Conus quercinus

<400> 604
Glx Gly Cys Cys Ser Asp Pro Ala Cys Ala Val Ser Asn Pro Asp Ile
1 5 10 15

Cys Gly Gly

<210> 605
<211> 17
<212> PRT
<213> Conus bandanus

<400> 605

Pro	Glu	Cys	Cys	Thr	His	Pro	Ala	Cys	His	Val	Ser	His	Pro	Glu	Leu
1				5					10					15	

Cys

<210> 606

<211> 17

<212> PRT

<213> *Conus marmoreus*

<400> 606

Pro	Glu	Cys	Cys	Thr	His	Pro	Ala	Cys	His	Val	Ser	Asn	Pro	Glu	Leu
1				5					10					15	

Cys

<210> 607

<211> 15

<212> PRT

<213> *Conus miles*

<400> 607

Cys	Cys	Asn	His	Pro	Ala	Cys	Ala	Gly	Lys	Asn	Ser	Asp	Leu	Cys
1				5					10					15

<210> 608

<211> 16

<212> PRT

<213> *Conus magus*

<400> 608

Gly	Cys	Cys	Tyr	His	Pro	Thr	Cys	His	Leu	Glu	His	Ser	Asn	Leu	Cys
1				5					10					15	

<210> 609

<211> 17

<212> PRT

<213> *Conus nobilis*

<400> 609

Gly	Cys	Cys	Glu	Arg	Pro	Pro	Cys	Arg	Trp	Gln	Asn	Pro	Asp	Leu	Cys
1				5					10					15	

Gly

<210> 610

<211> 17

<212> PRT

<213> *Conus atlanticus*

<400> 610

Thr	Cys	Cys	Ser	Arg	Pro	Thr	Cys	Arg	Met	Glu	Tyr	Pro	Glu	Leu	Cys
1				5					10					15	

Gly

<210> 611

<211> 21

<212> PRT

<213> Conus quercinus

<400> 611

Asn Glu Cys Cys Asp Asn Pro Pro Cys Lys Ser Ser Asn Pro Asp Leu
1 5 10 15

Cys Asp Trp Arg Ser
20

<210> 612

<211> 16

<212> PRT

<213> Conus leopardus

<400> 612

Cys Cys Ser Asn Pro Ala Cys Asn Arg Tyr Asn Pro Ala Ile Cys Asp
1 5 10 15

<210> 613

<211> 17

<212> PRT

<213> Conus emaciatus

<400> 613

Asp Cys Cys Asn Phe Pro Ala Cys Ala Ala Ser Asn Pro Gly Leu Cys
1 5 10 15

Thr

<210> 614

<211> 14

<212> PRT

<213> Conus victor

<400> 614

Cys Cys Ser Ser Pro Pro Cys Phe Ala Ser Asn Pro Ala Cys
1 5 10

<210> 615

<211> 17

<212> PRT

<213> Conus cinereus gubba

<400> 615

Gly Gly Cys Cys Ser Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys
1 5 10 15

Ala

<210> 616

<211> 15

<212> PRT

<213> Conus flavidus

<400> 616

Gly Cys Cys Ser Asn Pro Pro Cys Ser Tyr Leu Asn Pro Ala Cys
1 5 10 15

<210> 617

<211> 16

<212> PRT

<213> *Conus emaciatus*

<400> 617

Asp Cys Cys Ser Asp Pro Pro Cys Ala His Asn Asn Pro Asp Cys Arg
1 5 10 15

<210> 618

<211> 17

<212> PRT

<213> *Conus generalis*

<400> 618

Gly Cys Cys Ser Asn Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys
1 5 10 15

Asn

<210> 619

<211> 25

<212> PRT

<213> *Conus wittigi*

<400> 619

Asp Glu Cys Cys Ala His Pro Ser Cys Trp Lys Ala Glu Asp Leu Ile
1 5 10 15

Cys Thr Asn Gln Arg Arg Arg Thr Leu
20 25

<210> 620

<211> 20

<212> PRT

<213> *Conus characteristicus*

<400> 620

Gly Cys Cys Ala Ile Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys
1 5 10 15

Gly Gly Ile Ser
20

<210> 621

<211> 19

<212> PRT

<213> *Conus betulinus*

<400> 621

Ser Ala Thr Cys Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala Tyr Pro Glu
1 5 10 15

Ser Cys Leu

<210> 622

<211> 6

<212> PRT

<213> *Conus magus*

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Xaa is gamma-carboxy-Glu

<400> 622

Val Tyr Xaa Thr His Pro

1 5

<210> 623

<211> 14

<212> PRT

<213> Conus striatus

<400> 623

Trp Ser Trp Arg Met Gly Asn Gly Asp Arg Arg Ser Asp Gln

1 5 10

<210> 624.

<211> 11

<212> PRT

<213> Conus quercinus

<400> 624

Asp Cys Gln Pro Cys Gly His Asn Val Cys Cys

1 5 10

<210> 625

<211> 29

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa is gamma-carboxy-Glu

<400> 625

Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Tyr Cys

1 5 10 15

Ala Lys Gly Ile Ala Lys Glu Phe Cys Asn Cys Pro Asp

20 25

<210> 626

<211> 6

<212> PRT

<213> Conus magus

<400> 626

Arg Pro Lys Asn Ser Trp

1 5

<210> 627

<211> 7

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(7)

<223> Xaa is hydroxy-Pro

<400> 627

Ala Arg Xaa Lys Asn Ser Trp
1 5

<210> 628

<211> 6

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Xaa is hydroxy-Pro

<400> 628

Arg Xaa Lys Asn Ser Trp
1 5

<210> 629

<211> 71

<212> PRT

<213> Conus geographus

<400> 629

Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
1 5 10 15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
20 25 30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp
35 40 45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
50 55 60

Pro Cys Gly Gly Ala Ala Leu
65 70

<210> 630

<211> 65

<212> PRT

<213> Conus geographus

<400> 630

Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg Ser Ser
1 5 10 15

Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys Thr Pro
20 25 30

Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe His Gln
35 40 45

Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys Arg Asp
50 55 60

Ala
65

<210> 631
 <211> 60
 <212> PRT
 <213> *Conus geographus*

<400> 631
 Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Glu
 1 5 10 15
 Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Glu Trp
 20 25 30
 Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly Gly Ala
 35 40 45
 Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu Cys
 50 55 60

<210> 632
 <211> 43
 <212> PRT
 <213> *Conus radiatus*

<400> 632
 Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val Gly Glu Thr Tyr Gln
 1 5 10 15
 Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe Asp Leu Ala Thr Cys
 20 25 30
 Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
 35 40

<210> 633
 <211> 86
 <212> PRT
 <213> *Conus striatus*

<400> 633
 Ser Gly Pro Ala Asp Cys Cys Arg Met Lys Glu Cys Cys Thr Asp Arg
 1 5 10 15
 Val Asn Glu Cys Leu Gln Arg Tyr Ser Gly Arg Glu Asp Lys Phe Val
 20 25 30
 Ser Phe Cys Tyr Gln Glu Ala Thr Val Thr Cys Gly Ser Phe Asn Glu
 35 40 45
 Ile Val Gly Cys Cys Tyr Gly Tyr Gln Met Cys Met Ile Arg Val Val
 50 55 60
 Lys Pro Asn Ser Leu Ser Gly Ala His Glu Ala Cys Lys Thr Val Ser
 65 70 75 80
 Cys Gly Asn Pro Cys Ala
 85

<210> 634
 <211> 24

<212> PRT

<213> *Conus purpurascens*

<400> 634

Asp Cys Cys Gly Val Lys Leu Glu Met Cys His Pro Cys Leu Cys Asp
 1 5 10 15

Asn Ser Cys Lys Asn Tyr Gly Lys
 20

<210> 635

<211> 36

<212> PRT

<213> *Conus geographus*

<400> 635

Gly Glu Pro Ile Pro Thr Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys
 1 5 10 15

Asp Pro Ser Cys Trp Val Lys Val Lys Asp Phe Gln Cys Pro Gly Ala
 20 25 30

Ser Pro Pro Asn
 35

<210> 636

<211> 16

<212> PRT

<213> *Conus generalis*

<400> 636

Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

<210> 637

<211> 20

<212> PRT

<213> *Conus tessulatus*

<400> 637

Asp Gly Cys Pro Pro His Pro Val Pro Gly Met His Lys Cys Met Cys
 1 5 10 15

Thr Asn Thr Cys
 20

<210> 638

<211> 84

<212> PRT

<213> *Conus radiatus*

<400> 638

His Pro Thr Lys Pro Cys Met Tyr Cys Ser Phe Gly Gln Cys Val Gly
 1 5 10 15

Pro His Ile Cys Cys Gly Pro Thr Gly Cys Glu Met Gly Thr Ala Glu
 20 25 30

Ala Asn Met Cys Ser Glu Glu Asp Glu Asp Pro Ile Pro Cys Gln Val
 35 40 45

Phe Gly Ser Asp Cys Ala Leu Asn Asn Pro Asp Asn Ile His Gly His
50 55 60

Cys Val Ala Asp Gly Ile Cys Cys Val Asp Asp Thr Cys Thr Thr His
65 70 75 80

Leu Gly Cys Leu